Cook, L
08/837301

(FILE 'CAPLUS' ENTERED AT 15:58:47 ON 02 AUG 1999)

=> d que

-key terms

L4 183866 SEA FILE=CAPLUS ABB=ON PLU=ON (POLYPEPTIDE OR POLYPROTE
IN OR POLY(W)(PROTEIN OR PEPTIDE) OR AMINO) AND (RECEPTOR
OR LIGAND OR ANTIGEN OR ANTIBOD? OR ENZYME)
L6 11 SEA FILE=CAPLUS ABB=ON PLU=ON L4 AND ((SOC OR HOC)(S)CA
PSID OR (HIGH? OR SMALL?)(2W)CAPSID)

=> d 1-11 .bevstr1

L6 ANSWER 1 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1998:591346 CAPLUS
DOCUMENT NUMBER: 129:314304
TITLE: A viral gene that activates lytic cycle expression of Kaposi's sarcoma-associated herpesvirus
AUTHOR(S): Sun, Ren; Lin, Su-Fang; Gradoville, Lyndle; Yuan, Yan; Zhu, Fanxiu; Miller, George
CORPORATE SOURCE: Departments of Molecular Biophysics and Biochemistry, Genetics, Pediatrics, and Epidemiology and Public Health, Yale University School of Medicine, New Haven, CT, 06520, USA
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1998), 95(18), 10866-10871
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Herpesviruses exist in two states, latency and a lytic productive cycle. Here we identify an immediate-early gene encoded by Kaposi's sarcoma-assocd. herpesvirus (KSHV)/human herpesvirus eight (HHV8) that activates lytic cycle gene expression from the latent viral genome. The gene is a homolog of Rta, a transcriptional activator encoded by Epstein-Barr virus (EBV). KSHV/Rta activated KSHV early lytic genes, including virus-encoded interleukin 6 and polyadenylated nuclear RNA, and a late gene, **small** viral **capsid antigen**. In cells dually infected with Epstein-Barr virus and KSHV, each Rta activated only autologous lytic cycle genes. Expression of viral cytokines under control of the KSHV/Rta gene is likely to contribute to the pathogenesis of KSHV-assocd. diseases.
IT Interleukin 6
RL: BSU (Biological study, unclassified); BIOL (Biological study) (HHV8 early lytic gene for; viral gene that activates lytic cycle expression of Kaposi's sarcoma-assocd. herpesvirus)
IT Genes (microbial)
RL: BPR (Biological process); BIOL (Biological study); PROC

(Process)
(early lytic; viral gene that activates lytic cycle expression of Kaposi's sarcoma-assocd. herpesvirus)

IT Genes (microbial)
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(for polyadenylated nuclear RNA, early lytic; viral gene that activates lytic cycle expression of Kaposi's sarcoma-assocd. herpesvirus)

IT Human herpesvirus 8
(gene in; viral gene that activates lytic cycle expression of Kaposi's sarcoma-assocd. herpesvirus)

IT Genes (microbial)
Transcription factors
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(homolog of Rta; viral gene that activates lytic cycle expression of Kaposi's sarcoma-assocd. herpesvirus)

IT DNA sequences
(of Kaposi's sarcoma-assocd. herpesvirus genome fragments III and IV)

IT Protein sequences
(of Kaposi's sarcoma-assocd. herpesvirus genome fragments III and IV encoded proteins)

IT RNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(poly(A)-contg., early lytic gene for; viral gene that activates lytic cycle expression of Kaposi's sarcoma-assocd. herpesvirus)

IT **Antigens**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**small** viral **capsid**, late gene for; viral gene that activates lytic cycle expression of Kaposi's sarcoma-assocd. herpesvirus)

IT 183389-42-6 185072-49-5 185072-50-8 214609-78-6 214609-79-7 214609-80-0
RL: PRP (Properties)
(**amino** acid sequence; viral gene that activates lytic cycle expression of Kaposi's sarcoma-assocd. herpesvirus)

IT 214745-23-0 214745-24-1
RL: PRP (Properties)
(nucleotide sequence; viral gene that activates lytic cycle expression of Kaposi's sarcoma-assocd. herpesvirus)

L6 ANSWER 2 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1998:590311 CAPLUS
DOCUMENT NUMBER: 129:286551
TITLE: Phage T4 **SOC** and **HOC** display of biologically active, full-length proteins on

the viral **capsid**

AUTHOR(S): Ren, Zhao-Jun; Black, Lindsay W.
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Maryland School of Medicine, Baltimore, MD, 21201-1503, USA

SOURCE: Gene (1998), 215(2), 439-444
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The T4 phage **capsid** accessory protein genes **soc** and **hoc** have recently been developed for display of peptides and protein domains at high copy no. That biol. active and full-length foreign proteins can be displayed by fusion to **SOC** and **HOC** on the T4 **capsid** is demonstrated in this report. A 271-residue heavy and light chain fused IgG anti-EWL (egg white lysozyme) **antibody** was displayed in active form attached to the COOH-terminus of the **SOC capsid** protein, as demonstrated by lysozyme-agarose affinity chromatog. (> 100-fold increase in specific titer). **HOC** with NH2-terminal fused HIV-I CD4 **receptor** of 183 **amino** acids can be detected on the T4 outer **capsid** surface with human CD4 domain 1 and 2 monoclonal **antibodies**. The no. of mols. of each protein (10-40) bound per phage and their activity suggest that proteins can fold to native conformation and be displayed by **HOC** and **SOC** to allow binding and protein-protein interactions on the **capsid**.

IT CD4 (**antigen**)
RL: BUU (Biological use, unclassified); BIOL (Biological study);
USES (Uses)
(HIV-1; phage T4 **SOC** and **HOC** display of biol. active, full-length proteins on the viral **capsid**)

IT **Capsid** proteins
RL: BUU (Biological use, unclassified); BIOL (Biological study);
USES (Uses)
(**SOC** (**small** outer **capsid** protein) and **HOC** (**highly** antigenic outer **capsid** protein); phage T4 **SOC** and **HOC** display of biol. active, full-length proteins on the viral **capsid**)

IT IgG
RL: BUU (Biological use, unclassified); BIOL (Biological study);
USES (Uses)
(VH and VL fusion; phage T4 **SOC** and **HOC** display of biol. active, full-length proteins on the viral **capsid**)

IT Fusion proteins (chimeric proteins)
RL: BPN (Biosynthetic preparation); BPR (Biological process); BIOL

(Biological study); PREP (Preparation); PROC (Process)
(gene **hoc capsid** protein fused with CD4 **receptor**; phage T4 **SOC** and **HOC** display of biol. active, full-length proteins on the viral **capsid**)

IT Fusion proteins (chimeric proteins)
RL: BPN (Biosynthetic preparation); BPR (Biological process); BIOL (Biological study); PREP (Preparation); PROC (Process)
(gene **soc capsid** protein fused with mAb against EWL; phage T4 **SOC** and **HOC** display of biol. active, full-length proteins on the viral **capsid**)

IT Plasmid vectors
(pESS and pRSS and pCD4-**HOC**; phage T4 **SOC** and **HOC** display of biol. active, full-length proteins on the viral **capsid**)

IT **Capsid**
Coliphage T4
Phage display
(phage T4 **SOC** and **HOC** display of biol. active, full-length proteins on the viral **capsid**)

L6 ANSWER 3 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1997:730973 CAPLUS
DOCUMENT NUMBER: 128:44380
TITLE: Display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 capsid surface
AUTHOR(S): Jiang, Jennifer; Abu-Shilbayeh, Lara; Rao, Venigalla B.
CORPORATE SOURCE: Dep. Biology, Catholic Univ. America, Washington, DC, 20064, USA
SOURCE: Infect. Immun. (1997), 65(11), 4770-4777
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The exterior of bacteriophage T4 **capsid** is coated with two outer **capsid** proteins, **Hoc** (**highly** antigenic outer **capsid** protein; mol. mass, 40 kDa) and **Soc** (**small** outer **capsid** protein; mol. mass, 9 kDa), at sym. positions on the icosahedron (160 copies of **Hoc** and 960 copies of **Soc** per **capsid** particle). Both these proteins are nonessential for phage infectivity and viability and assemble onto the capsid surface after completion of capsid assembly. We developed a phage display system which allowed in-frame fusions of foreign DNA at a unique cloning site in the 5' end of hoc or soc. A DNA fragment corresponding to the 36-**amino**-acid PorA peptide from Neisseria meningitidis was cloned into the display vectors to generate fusions at the N

terminus of Hoc or Soc. The PorA-**Hoc** and PorA-**Soc** fusion proteins retained the ability to bind to the **capsid** surface, and the bound peptide was displayed in an accessible form as shown by its reactivity with specific monoclonal **antibodies** in an ELISA. By employing T4 genetic strategies, we show that more than one subtype-specific PorA peptide can be displayed on the capsid surface and that the peptide can also be displayed on a DNA-free empty capsid. Both the PorA-Hoc and PorA-Soc recombinant phages are highly immunogenic in mice and elicit strong antipeptide **antibody** titers even with a weak adjuvant such as Alhydrogel or no adjuvant at all. The data suggest that the phage T4 **hoc-soc** system is an attractive system for display of peptides on an icosahedral **capsid** surface and may emerge as a powerful system for construction of the next generation multicomponent vaccines.

IT Capsid
(DNA-free empty; display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 capsid surface)

IT Outer membrane proteins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(OMP1 (outer membrane protein 1); display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 capsid surface)

IT Fusion proteins (chimeric proteins)
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(PorA-**Hoc** and PorA-**Soc** fusion proteins retained the ability to bind to **capsid** surface; display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 **capsid** surface)

IT **Antigens**
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)
(PorA-**Hoc** and PorA-**Soc** recombinant phages are highly immunogenic in mice; display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 **capsid** surface)

IT Peptides, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(PorA; display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 capsid surface)

IT Coliphage T4
Neisseria meningitidis
Phage display
(display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 capsid surface)

IT Genes (microbial)

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(**hoc**, in-frame fusions of foreign DNA at a unique cloning site in 5' end of **hoc** or **soc**; display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 **capsid** surface)

IT Chimeric genes
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(in-frame fusions of foreign DNA at a unique cloning site in 5' end of **hoc** or **soc**; display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 **capsid** surface)

IT Genes (microbial)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(**soc**, in-frame fusions of foreign DNA at a unique cloning site in 5' end of **hoc** or **soc**; display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 **capsid** surface)

L6 ANSWER 4 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1997:503877 CAPLUS
DOCUMENT NUMBER: 127:189394
TITLE: Prevalence of Herpesvirus papio 2 in baboons and identification of immunogenic viral **polypeptides**
AUTHOR(S): Eberle, R.; Black, Darla H.; Blewett, Earl L.; White, Gary L.
CORPORATE SOURCE: Department of Infectious Diseases and Physiology, College of Veterinary Medicine, Oklahoma State University, Stillwater, OK, 74078-0353, USA
SOURCE: Lab. Anim. Sci. (1997), 47(3), 256-262
CODEN: LBASAE; ISSN: 0023-6764
PUBLISHER: American Association for Laboratory Animal Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The prevalence of Herpesvirus papio 2 (HVP2) in several groups of captive and wild-caught baboons was detd. by detection of anti-HVP2 **antibodies** in 133 sera of adult baboons. Over 90% of newly imported (wild-caught) adult olive baboons (Papio anubis) from Kenya and chacma baboons (P. ursinus) from South Africa were found to have anti-HVP2 titers. Similarly, approx. 85% of captive breeding colony baboons (P. anubis and P. cynocephalus) were seropos. for HVP2.

Infected animals were generally easily identifiable by ELISA because anti-HVP2 IgG titers in immune animals were usually high (16,000 to 64,000). There was little variation in the relative reactivity patterns of individual HVP2-immune sera when tested against herpes simplex viruses 1 and 2, monkey B virus, H. cercopithecus 2, and HVP2, or against different HVP2 strains. Also, differences were not detected between reactivity of olive and chacma baboon immune sera. Anal. of the **polypeptide** specificity of immune sera by Western blot identified four viral **antigens** that were consistent targets of immune sera. These **antigens** were the gB glycoprotein, a pair of unidentified glycoproteins of 80 to 100 kDa, the gD glycoprotein, and a series of **smaller capsid** proteins. Addnl. viral proteins were variably recognized by individual immune sera. The results of this study indicate that HVP2 is a common infection of baboons; there is little antigenic variation among HVP2 strains; and there are several HVP2 **antigens** that represent consistent targets of the anti-HVP2 immune response of baboons.

IT Glycoproteins (specific proteins and subclasses)
RL: BOC (Biological occurrence); BPR (Biological process); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(80,000-100,000-mol.-wt.; herpesvirus papio 2 infection prevalence and humoral immune response in baboons)

IT Glycoproteins (specific proteins and subclasses)
RL: BOC (Biological occurrence); BPR (Biological process); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(gB; herpesvirus papio 2 infection prevalence and humoral immune response in baboons)

IT Baboon
Baboon herpesvirus 2
Papio anubis
Papio cynocephalus
Papio ursinus
Viral infection
(herpesvirus papio 2 infection prevalence and humoral immune response in baboons)

IT **Antibodies**
Glycoprotein D
IgG
RL: BOC (Biological occurrence); BPR (Biological process); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(herpesvirus papio 2 infection prevalence and humoral immune response in baboons)

IT Capsid proteins
RL: BOC (Biological occurrence); BPR (Biological process); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(p40; herpesvirus papio 2 infection prevalence and humoral immune response in baboons)

L6 ANSWER 5 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1997:365648 CAPLUS
DOCUMENT NUMBER: 127:76761
TITLE: Five complete genomes of JC virus type 3 from Africans and African Americans
AUTHOR(S): Agostini, H. T.; Ryschkewitsch, C. F.; Brubaker, G. R.; Shao, J.; Stoner, G. L.
CORPORATE SOURCE: Laboratory of Experimental Neuropathology, National Institute of Neurological Disorders and Stroke, NIH, Bethesda, MD, USA
SOURCE: Arch. Virol. (1997), 142(4), 637-655
CODEN: ARVIDF; ISSN: 0304-8608
PUBLISHER: Springer
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The central demyelinating disease progressive multifocal leukoencephalopathy (PML) is caused by the human polyomavirus JC virus (JCV). JCV evolved as geog. based genotypes of which Type 3 is an African variant first characterized in HIV-1 pos. patients from Tanzania. This study reports the complete sequence of five JCV Type 3 strains. The entire JCV genome was PCR amplified from urine specimens of three African and two African-American individuals. The African consensus sequence was compared to the Type 1 and Type 2 prototype strains, JCV (Mad-1) and JCV(GS/B), resp. Type 3 differed in 2.2% of its coding region genome from JCV (Mad-1) and in 1.3% from JCV(GS/B). Within the coding region the sequence variation among the three types was **higher** in the **capsid** protein VP1 and in the regulatory protein large T **antigen** than in the agnoprotein or in VP2/3. Notable Type 3-specific changes were located at sites adjacent to the zinc finger motif and near the major donor and acceptor splice junctions of large T **antigen**. Four of the five urinary Type 3 strains had an unrearranged, archetypal regulatory region. African strain #309 showed a 10-bp deletion at a location similar to that previously described for #307 from Tanzania. The African-American Type 3 strain #312 was closely related to the African consensus sequence. The complete genome of a urinary JCV strain from another African-American male, previously reported as a possible Type 5, showed a sequence difference of only 0.52% from the Tanzanian consensus and has been reclassified as a subtype of Type 3.

IT Proteins (specific proteins and subclasses)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(agno-; five complete genomes of JC virus type 3 from Africans and African Americans)

IT DNA sequences
Genomes
Protein sequences

(five complete genomes of JC virus type 3 from Africans and African Americans)

IT Large T **antigen**
Protein VP1
Protein VP2
Protein VP3
Small t **antigen**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(five complete genomes of JC virus type 3 from Africans and African Americans)

IT Genes (microbial)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(for agnoprotein; five complete genomes of JC virus type 3 from Africans and African Americans)

IT Genes (microbial)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(for large T **antigen**; five complete genomes of JC virus type 3 from Africans and African Americans)

IT Genes (microbial)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(for protein VP1; five complete genomes of JC virus type 3 from Africans and African Americans)

IT Genes (microbial)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(for protein VP2; five complete genomes of JC virus type 3 from Africans and African Americans)

IT Genes (microbial)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(for protein VP3; five complete genomes of JC virus type 3 from Africans and African Americans)

IT Genes (microbial)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(for small T **antigen**; five complete genomes of JC virus type 3 from Africans and African Americans)

IT Brain diseases
(progressive multifocal leukoencephalopathy; five complete genomes of JC virus type 3 from Africans and African Americans)

IT Genetic elements
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(regulatory region; five complete genomes of JC virus type 3 from Africans and African Americans)

IT JC virus
(type 3; five complete genomes of JC virus type 3 from Africans and African Americans)
IT 84615-96-3, **Antigen** t (JC virus reduced) 191618-30-1, Agnoprotein (JC virus 3 strain 308) 191618-31-2, Protein VP2 (JC virus 3 strain 308) 191618-32-3, Protein VP3 (JC virus 3 strain 308) 191618-33-4, Large T **antigen** (JC virus 3 strain 308) 191809-24-2, Protein VP1 (JC virus 3 strain 308) 191809-25-3, Small t **antigen** (JC virus 3 strain 308) 191809-26-4, Agnoprotein (JC virus 3 strain 311) 191809-27-5, Protein VP2 (JC virus 3 strain 311) 191809-28-6, Protein VP3 (JC virus 3 strain 311) 191809-29-7, Large T **antigen** (JC virus 3 strain 311)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(**amino** acid sequence; five complete genomes of JC virus type 3 from Africans and African Americans)
IT 185926-16-3, GenBank U73178 185926-17-4, GenBank U73500 185926-18-5, GenBank U73501 185926-19-6, GenBank U73502
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; five complete genomes of JC virus type 3 from Africans and African Americans)

L6 ANSWER 6 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1997:185018 CAPLUS
DOCUMENT NUMBER: 126:292275
TITLE: Identification, expression, and immunogenicity of Kaposi's sarcoma-associated herpesvirus-encoded **small** viral **capsid antigen**
AUTHOR(S): Lin, Su-Fang; Sun, Ren; Heston, Lee; Gradoville, Lyn; Shedd, Duane; Haglund, Karl; Rigsby, Michael; Miller, George
CORPORATE SOURCE: Dep. Mol. Biophys. & Biochem., Yale Univ. Sch. Med., New Haven, CT, 06520, USA
SOURCE: J. Virol. (1997), 71(4), 3069-3076
CODEN: JOVIAM; ISSN: 0022-538X
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors describe a recombinant **antigen** for use in serol. tests for **antibodies** to Kaposi's sarcoma (KS)-assocd. herpesvirus (KSHV). The cDNA for a **small** viral **capsid antigen** (sVCA) was identified by immunoscreening of a library prepd. from the BC-1 body cavity lymphoma cell line induced into KSHV lytic gene expression by sodium butyrate. The cDNA specified a 170-**amino**-acid peptide with homol. to **small** viral **capsid** proteins

encoded by the BFRF3 gene of Epstein-Barr virus and the ORF65 gene of herpesvirus saimiri. KSHV sVCA was expressed from a 0.85-kb mRNA present late in lytic KSHV replication in BC-1 cells. This transcript was sensitive to phosphonoacetic acid and phosphonoformic acid, inhibitors of herpesvirus DNA replication. KSHV sVCA expressed in mammalian cells or Escherichia coli or translated in vitro was recognized as an **antigen** by antisera from KS patients. Rabbit antisera raised to KSHV sVCA expressed in E. coli detected a 22-kDa protein in KSHV-infected human B cells. Overexpressed KSHV sVCA purified from E. coli and used as an **antigen** in immunoblot screening assay did not cross-react with EBV BFRF3. **Antibodies** to sVCA were present in 89% of 47 human immunodeficiency virus (HIV)-pos. patients with KS, in 20% of 54 HIV-pos. patients without KS, but in none of 122 other patients including children born to HIV-serpos. mothers and patients with hemophilia, autoimmune disease, or nasopharyngeal carcinoma. Low-titer **antibody** was detected in three sera from 28 healthy subjects. **Antibodies** to recombinant sVCA correlate with KS in high-risk populations. Recombinant sVCA can be used to exam. the seroepidemiol. of infection with KSHV in the general population.

IT B cell (lymphocyte)
DNA replication
DNA sequences
Gene expression
Human herpesvirus 8
Immunity
Immunodiagnosis
Protein sequences
Transcription (genetic)
Viral infection
(cDNA sequence, expression in human and lab. animal cells, and immunogenicity of Kaposi's sarcoma-assocd. herpesvirus-encoded **small** viral **capsid antigen** and use in serol. tests for infection)

IT **Antibodies**
RL: ANT (Analyte); BOC (Biological occurrence); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(cDNA sequence, expression in human and lab. animal cells, and immunogenicity of Kaposi's sarcoma-assocd. herpesvirus-encoded **small** viral **capsid antigen** and use in serol. tests for infection)

IT mRNA
RL: BOC (Biological occurrence); BPR (Biological process); MFM (Metabolic formation); PRP (Properties); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence); PROC (Process)
(cDNA sequence, expression in human and lab. animal cells, and immunogenicity of Kaposi's sarcoma-assocd. herpesvirus-encoded

small viral **capsid antigen** and use in
serol. tests for infection)
IT Genes (animal)
RL: BOC (Biological occurrence); BPR (Biological process); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(cDNA sequence, expression in human and lab. animal cells, and immunogenicity of Kaposi's sarcoma-assocd. herpesvirus-encoded **small** viral **capsid antigen** and use in serol. tests for infection)
IT Human immunodeficiency virus
(cDNA sequence, expression in human and lab. animal cells, and immunogenicity of Kaposi's sarcoma-assocd. herpesvirus-encoded **small** viral **capsid antigen** and use in serol. tests for infection in relation to)
IT **Antigens**
Capsid proteins
RL: ARG (Analytical reagent use); BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(sVCA (**small** viral **capsid antigen**);
cDNA sequence, expression in human and lab. animal cells, and immunogenicity of Kaposi's sarcoma-assocd. herpesvirus-encoded **small** viral **capsid antigen** and use in serol. tests for infection)
IT 185072-71-3
RL: PRP (Properties)
(**amino** acid sequence; cDNA sequence, expression in human and lab. animal cells, and immunogenicity of Kaposi's sarcoma-assocd. herpesvirus-encoded **small** viral **capsid antigen** and use in serol. tests for infection)
IT 187764-12-1, GenBank U50141
RL: PRP (Properties)
(nucleotide sequence; cDNA sequence, expression in human and lab. animal cells, and immunogenicity of Kaposi's sarcoma-assocd. herpesvirus-encoded **small** viral **capsid antigen** and use in serol. tests for infection)

L6 ANSWER 7 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1992:77606 CAPLUS
DOCUMENT NUMBER: 116:77606
TITLE: The unique sequence of the herpes simplex virus 1 L component contains an additional translated open reading frame designated UL49.5
AUTHOR(S): Barker, David E.; Roizman, Bernard
CORPORATE SOURCE: Marjorie B. Kovler Viral Oncol. Lab., Univ. Chicago, Chicago, IL, 60637, USA
SOURCE: J. Virol. (1992), 66(1), 562-6
Searcher : Shears 308-4994

CODEN: JOVIAM; ISSN: 0022-538X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors present evidence for the existence of an addnl. herpes simplex virus 1 gene designated UL49.5. The sequence, located between genes UL49 and UL50, predicts a hydrophobic protein with 91 **amino** acids. Attempts to delete UL49.5 were not successful. To demonstrate that UL49.5 is expressed, two recombinant viruses were made. First, an oligonucleotide encoding a 15-**amino** -acid epitope known to react with a monoclonal **antibody** were inserted in frame. This gene, consisting of the authentic promoter and chimeric coding domain, was inserted into the thymidine kinase gene of wild-type virus and in infected cells expressed a protein which reacted with the monoclonal **antibody**. The second recombinant virus contained a 5' UL49.5-thymidine kinase fusion gene. The protein expressed by this virus confirmed that the first methionine codon of UL49.5 served as the initiating codon. The predicted **amino** acid sequence of UL49.5 is consistent with the known properties of NC-7, a **small capsid** protein whose gene has not been previously mapped. A homol. of UL49.5 is present in the genome of varicella-zoster virus, located between homologs of UL49 and UL50.
IT Proteins, specific or class
RL: BIOL (Biological study)
(NC-7, gene for, of herpes simplex virus 1 L component)
IT Gene, microbial
RL: BIOL (Biological study)
(UL49.5, for protein NC-7, of herpes simplex virus 1 L component, mapping of)
IT Genetic mapping
(of gene UL49.5 of herpes simplex virus 1 L component)
IT Virus, animal
(herpes simplex 1, L component of, gene for protein NC-7 on)
IT Virus, animal
(varicella-zoster, herpes simplex virus 1 gene UL49.5 homol. to ORF8.5 of)

L6 ANSWER 8 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1988:34539 CAPLUS
DOCUMENT NUMBER: 108:34539
TITLE: Isolation and antigenic characterization of dense particles of swine enteroviruses
AUTHOR(S): Urakawa, Toyohiko; Hamada, Nobuyuki; Shingu, Masahisa
CORPORATE SOURCE: Sch. Med., Kurume Univ., Kurume, 830, Japan
SOURCE: Kurume Med. J. (1987), 34(2), 65-73
CODEN: KRMJAC; ISSN: 0023-5679
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Dense (1.45-1.47 g/cm3) particles were isolated from HeLa cells infected with swine enteroviruses and coxsackievirus type B5. These dense particles had important properties which were different from those of poliovirus and other picornaviruses; for instance, they could be isolated under various conditions of virus growth. The **smallest capsid polypeptide**, VP4, was not detected by SDS-PAGE anal. The dense particles were noninfectious and showed H antigenicity by a modified **enzyme** immunoassay. Judging from these properties, dense particles might be equiv. to A particles. These findings suggest that the VP4 **polypeptide** is responsible for the conformational stabilization of the intact virion.

IT **Antigens**
RL: BIOL (Biological study)
(of swine enterovirus dense particles)

IT Virus, animal
(Coxsackie B5, dense particles of, isolation and antigenic characterization of)

IT Proteins, specific or class
RL: PROC (Process)
(VP4, of dense particles of swine enterovirus, antigenic characterization of)

IT Virus, animal
(porcine entero-, dense particles of, isolation and antigenic characterization of)

L6 ANSWER 9 OF 11 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER: 1981:137592 CAPLUS
DOCUMENT NUMBER: 94:137592
TITLE: Antigenic and structural relatedness among non-capsid and capsid **polypeptides** of polioviruses belonging to different serotypes
AUTHOR(S): Romanova, Lyudmila I.; Tolskaya, Elena A.; Agol, Vadim I.
CORPORATE SOURCE: Inst. Poliomyelitis Viral Encephalitides, Moscow State Univ., Moscow, 117234, USSR
SOURCE: J. Gen. Virol. (1981), 52(2), 279-89
CODEN: JGVIAY; ISSN: 0022-1317
DOCUMENT TYPE: Journal
LANGUAGE: English

AB **Antibodies** were raised by immunization of Macaca fascicularis monkeys with exts. of M. fascicularis kidney cells sep. infected with 1 of the 3 poliovirus serotypes. The **antibodies** were strictly type-specific in the neutralization test but formed immune complexes adsorbable on Staphylococcus aureus, Cowan I strain, cells, with heterotypic as well as homotypic virus-specific **polypeptides** being present in exts. from the virus-infected cells. The presence of intertypic antigenic determinants was demonstrated by this technique on both the

noncapsid and capsid poliovirus **polypeptides**. Structural variations of the poliovirus **polypeptides** were studied by analyzing the products of their partial proteolysis. Noncapsid **polypeptides** encoded in the central portion of the virus genome (**polypeptides** 5b and X) as well as in the 3'-terminal region (NCVP2 and NCVP4) were **highly** conserved, whereas **capsid polypeptides** VP1, VP2, and VP3, which are encoded in the 5'-terminal region of the virus RNA, displayed a much greater variability.

IT **Antigens**
RL: BIOL (Biological study)
(determinants, of capsid and noncapsid proteins of poliovirus serotypes)

IT Proteins
RL: BIOL (Biological study)
(of poliovirus serotypes, antigenic and structural relatedness of)

IT Virus, animal
(polio-, proteins of serotypes of, antigenic and structural relatedness of)

L6 ANSWER 10 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1977:117359 CAPLUS
DOCUMENT NUMBER: 86:117359
TITLE: The two dispensable structural proteins (**soc** and **hoc**) of the T4 phage **capsid**; their purification and properties, isolation and characterization of the defective mutants, and their binding with the defective heads in vitro
AUTHOR(S): Ishii, Tetsuro; Yanagida, Mitsuhiro
CORPORATE SOURCE: Fac. Sci., Kyoto Univ., Kyoto, Japan
SOURCE: J. Mol. Biol. (1977), 109(4), 487-514
CODEN: JMOBAK
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Two classes of T4 **capsid** proteins, called **soc** and **hoc**, were **highly** purified from **capsids** by a general procedure for fractionating the **capsid polypeptides**. Their **amino** acid compns., antigenicities, and states in the infected bacteria were studied. The no. of **soc** protein mols. (mol. wt. 10,000) in the **capsid** is approx. equiv. to the no. of P23* mols., another major protein. The no. of hoc protein mols. (mol. wt. 40,000) is lower, being .apprx.1/8 of that of P23* mols. Electron microscopic observations of **antibody**-bound capsids suggest that these proteins are distributed over the entire surface of the heads. Mutant phages missing either soc or hoc or both proteins were isolated; these mutants are viable, and the proteins are

nonessential for phage growth. These mutants have normal morphol. but are different from the wild type in several physico-chem. properties. The soc-defective phages are inactivatedat pH 10.6, although the wild-type phages are resistant. The mutant phages are heavier in d. than the wild type. A gene located between genes 39 and 56 is involved in the prodn. of the soc protein. Binding reactions in vitro of a large no. of soc or hoc mols. to defective heads were demonstrated, which might mimic the maturation of the heads in vivo. The nature of these assocn. ractions was investigated quant. by using the specific characteristics of the mutants.

IT Proteins
RL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)
(of phage T4)

IT Virus, bacterial
(T4, proteins of, nonessential)

L6 ANSWER 11 OF 11 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1972:69973 CAPLUS
DOCUMENT NUMBER: 76:69973
TITLE: Early interaction of rhinoviruses with host cells
AUTHOR(S): Lonberg-Holm, L.; Korant, B. D.
CORPORATE SOURCE: Cent. Res. Dep., E. I. du Pont de Nemours and Co., Wilmington, Del., USA
SOURCE: J. Virol. (1972), 9(1), 29-40
CODEN: JOVIAM
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The rate of attachment of type 2 virions to suspensions of HeLa cells is much greater than that of type 14, but the no. of **receptor** sites per cell is similar for each type. The **receptor** sites may be partly satd. with excess virions; attachment is greatly decreased after .apprx.104 particles have been taken up per cell. A lack of satn. of type 14 **receptors** by excess type 2 indicates that their **receptor** sites are sep. on the cell surface. Excess of type 2 blocks attachment of type 1A, however, and excess of type 14 blocks type 51. Attachment of the human rhinoviruses is temp.-dependent with a Q10 of 2.7. The eclipse reaction is also temp.-dependent. At 34.5.degree. the irreversible eclipse of cell-assocd. rhinovirus type 2 requires only a few min, whereas the rate of eclipse of cell-assocd. type 14 is considerably slower. The eclipse product of type 2 rhinovirus has been recovered from infected cells. It sediments at .apprx.90% of the rate of the infective virons and is missing virus **polypeptide** 4 (the **smallest** of the **capsid polypeptides**). Upon being subjected to CsCl gradient centrifugation, virus **polypeptide** 2 is also lost but the

product still contains RNA bands at .apprx.1.45 g/cc.
IT Heat, biological effects
(on rhino virus interaction with host cells)
IT Virus, animal
(rhino-, interaction of, with hosts of)

=> d his l7-; d 1-27 ibib abs

(FILE 'MEDLINE, BIOSIS, EMBASE, LIFESCI, BIOTECHDS, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, PROMT' ENTERED AT 16:06:13 ON 02 AUG 1999)
L7 58 S L6
L8 27 DUP REM L7 (31 DUPLICATES REMOVED)

L8 ANSWER 1 OF 27 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 1999169196 MEDLINE
DOCUMENT NUMBER: 99169196
TITLE: Human serum **antibodies** to a major defined epitope of human herpesvirus 8 **small** viral **capsid antigen**.
AUTHOR: Tedeschi R; De Paoli P; Schulz T F; Dillner J
CORPORATE SOURCE: Microbiology and Tumor Biology Center, Karolinska Institute, Stockholm,Sweden.. micro@ets.it
SOURCE: JOURNAL OF INFECTIOUS DISEASES, (1999 Apr) 179 (4) 1016-20.
Journal code: IH3. ISSN: 0022-1899.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199906
ENTRY WEEK: 19990604
AB The major **antibody**-reactive epitope of the **small** viral **capsid antigen** (sVCA) of human herpesvirus 8 (HHV-8) was defined by use of overlapping peptides. Strong IgG reactivity was found among approximately 50% of 44 human immunodeficiency virus-positive or -negative patients with Kaposi's sarcoma and 13 subjects who were seropositive by immunofluorescence assay (IFA) for the latent HHV-8 nuclear **antigen**. Only 1 of 106 subjects seronegative for both lytic and latent HHV-8 **antigens** and 10 of 81 subjects IFA-seropositive only for the lytic HHV-8 **antigen** had strong IgG reactivity to this epitope. Among 534 healthy Swedish women, only 1.3% were strongly seropositive. Comparison of the peptide-based and purified sVCA protein-based ELISAs found 55% sensitivity and 98% specificity. However, only 1 of 452 serum samples from healthy women was positive in both tests. In conclusion, the defined sVCA epitope was a specific, but not very sensitive, serologic marker of active HHV-8 infection. Such infection appears to be rare among Swedish women, even with sexual risk-taking behavior.

Searcher : Shears 308-4994

L8 ANSWER 2 OF 27 EMBASE COPYRIGHT 1999 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 1999210476 EMBASE
TITLE: Analysis of capsid portal protein and terminase functional domains: Interaction sites required for DNA packaging in bacteriophage T4.
AUTHOR: Lin H.; Rao V.B.; Black L.W.
CORPORATE SOURCE: L.W. Black, Dept. Biochemistry Molecular Biology, University of Maryland at Baltimore, Baltimore, MD 21201-1503, United States. lblack@umaryland.edu
SOURCE: Journal of Molecular Biology, (4 Jun 1999) 289/2 (249-260).
Refs: 40
ISSN: 0022-2836 CODEN: JMOBAK
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Bacteriophage DNA packaging results from an ATP-driven translocation of concatemeric DNA into the prohead by the phage terminase complexed with the portal vertex dodecamer of the prohead. Functional domains of the bacteriophage T4 terminase and portal gene 20 product (gp20) were determined by mutant analysis and sequence localization within the structural genes. Interaction regions of the portal vertex and large terminase subunit (gp17) were determined by genetic (terminase-portal intergenic suppressor mutations), biochemical (column retention of gp17 and inhibition of in vitro DNA packaging by gp20 peptides), and immunological (co-immunoprecipitation of polymerized gp20 peptide and gp17) studies. The specificity of the interaction was tested by means of a phage T4 **HOC** (**highly** antigenic outer **capsid** protein) display system in which wild-type, cs20, and scrambled portal peptide sequences were displayed on the **HOC** protein of phage T4. Binding affinities of these recombinant phages as determined by the retention of these phages by a His-tag immobilized gp17 column, and by co-inununoprecipitation with purified terminase supported the specific nature of the portal protein and terminase interaction sites. In further support of specificity, a gp20 peptide corresponding to a portion of the identified site inhibited packaging whereas the scrambled sequence peptide did not block DNA packaging in vitro. The portal interaction site is localized to 28 residues in the central portion of the linear sequence of gp20 (524 residues). As judged by two pairs of intergenic portal-terminase suppressor mutations, two separate regions of the terminase large subunit gp17 (central and COOH-terminal) interact through hydrophobic contacts at the portal site. Although the terminase apparently interacts with this gp20 portal peptide, polyclonal

antibody against the portal peptide appears unable to access it in the native structure, suggesting intimate association of gp20 and gp17 possibly internalizes terminase regions within the portal in the packasome complex. Both similarities and differences are seen in comparison to analogous sites which have been identified in phages T3 and .lambda..

L8 ANSWER 3 OF 27 MEDLINE
ACCESSION NUMBER: 1998393737 MEDLINE
DOCUMENT NUMBER: 98393737
TITLE: A viral gene that activates lytic cycle expression of Kaposi's sarcoma-associated herpesvirus.
AUTHOR: Sun R; Lin S F; Gradoville L; Yuan Y; Zhu F; Miller G
CORPORATE SOURCE: Departments of Molecular Biophysics and Biochemistry, Genetics, Pediatrics, and Epidemiology and Public Health, Yale University School of Medicine, New Haven, CT 06520, USA.
CONTRACT NUMBER: CA70036 (NCI)
CA12055 (NCI)
T32CA09159 (NCI)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1998 Sep 1) 95 (18) 10866-71.
Journal code: PV3. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
OTHER SOURCE: GENBANK-U71368; GENBANK-U71367
ENTRY MONTH: 199812
ENTRY WEEK: 19981201
AB Herpesviruses exist in two states, latency and a lytic productive cycle. Here we identify an immediate-early gene encoded by Kaposi's sarcoma-associated herpesvirus (KSHV)/human herpesvirus eight (HHV8) that activates lytic cycle gene expression from the latent viral genome. The gene is a homologue of Rta, a transcriptional activator encoded by Epstein-Barr virus (EBV). KSHV/Rta activated KSHV early lytic genes, including virus-encoded interleukin 6 and polyadenylated nuclear RNA, and a late gene, **small** viral **capsid antigen**. In cells dually infected with Epstein-Barr virus and KSHV, each Rta activated only autologous lytic cycle genes. Expression of viral cytokines under control of the KSHV/Rta gene is likely to contribute to the pathogenesis of KSHV-associated diseases.

L8 ANSWER 4 OF 27 EMBASE COPYRIGHT 1999 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 1998034341 EMBASE
TITLE: Evidence of viral capsid dynamics using limited proteolysis mass spectrometry.

AUTHOR: Bothnor B.; Dong X.F.; Bibbs L.; Johnson J.E.; Siuzdak G.
CORPORATE SOURCE: J.E. Johnson, Dept. of Molec. Biology/Chemistry, Scripps Research Institute, San Diego, CA 92037, United States. jackj@scripps.edu
SOURCE: Journal of Biological Chemistry, (1998) 273/2 (673-676).
Refs: 18
ISSN: 0021-9258 CODEN: JBCHA3
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Virus particles are stable yet exhibit highly dynamic character given the events that shape their life cycle. Isolated from their hosts, the nucleoprotein particles are macromolecules that can be crystallized and studied by x-ray diffraction. During assembly, maturation and entry, however, they are highly dynamic and display remarkable plasticity. These dynamic properties can only be inferred from the x-ray structure and must be studied by methods that are sensitive to mobility. We have used matrix-assisted laser desorption/ionization mass spectrometry combined with time resolved, limited proteolysis (Cohen, S. L., Ferre-D'Amare, A. R., Burley, S. K., and Chait, B. T. (1995) Protein Sci. 4, 10881099; Kriwacki, R. W., Wu, J., Tennant, T., Wright, P. E., and Siuzdak, G. (1997) J. Chromatogr. 777, 23-30; Kriwacki, R. W., Wu, J., Siuzdak, G., and Wright, P. E. (1996) J. Am. Chem. **Soc**. 118, 5320-5321) to examine the vital **capsid** of flock house virus. Employing less than 10 .mu.g of virus, time course digestion products were assigned to **polypeptides** of the subunit. Although surface regions in the three- dimensional structure were susceptible to cleavage on extended exposure to the protease, the first digestion products were invariably from parts of the subunit that are internal to the x-ray structure. Regions in the N- and C- terminal portions of the subunit, located within the shell in the x-ray structure, but implicated in RNA neutralization and RNA release and delivery, respectively, were the most susceptible to cleavage demonstrating transient exposure of these **polypeptides** to the vital surface.

L8 ANSWER 5 OF 27 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 1998382537 MEDLINE
DOCUMENT NUMBER: 98382537
TITLE: Phage T4 **SOC** and **HOC** display of biologically active, full-length proteins on the viral **capsid**.
AUTHOR: Ren Z; Black L W
CORPORATE SOURCE: Department of Biochemistry, Molecular Biology,

University of Maryland School of Medicine, Baltimore, MD 21201-1503, USA.
CONTRACT NUMBER: AI11676 (NIAID)
SOURCE: GENE, (1998 Jul 30) 215 (2) 439-44.
Journal code: FOP. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199812
ENTRY WEEK: 19981201

AB The T4 phage **capsid** accessory protein genes **soc** and **hoc** have recently been developed for display of peptides and protein domains at high copy number (Ren et al., 1996. Protein Science 5, 1833-1843; Ren et al., 1997. Gene 195, 303-311). That biologically active and full-length foreign proteins can be displayed by fusion to **SOC** and **HOC** on the T4 **capsid** is demonstrated in this report. A 271-residue heavy and light chain fused IgG anti-EWL (egg white lysozyme) **antibody** was displayed in active form attached to the COOH-terminus of the **SOC capsid** protein, as demonstrated by lysozyme-agarose affinity chromatography (>100-fold increase in specific titer). **HOC** with NH2-terminal fused HIV-I CD4 **receptor** of 183 **amino** acids can be detected on the T4 outer **capsid** surface with human CD4 domain 1 and 2 monoclonal **antibodies**. The number of molecules of each protein (10-40) bound per phage and their activity suggest that proteins can fold to native conformation and be displayed by **HOC** and **SOC** to allow binding and protein-protein interactions on the **capsid**.

L8 ANSWER 6 OF 27 BIOTECHDS COPYRIGHT 1999 DERWENT INFORMATION LTD
ACCESSION NUMBER: 99-00537 BIOTECHDS
TITLE: Construction of a super vaccine using bacteriophage T4; multicomponent phage T4 vaccine construction (conference abstract)
AUTHOR: Rao V B; O'Brein M; Jiang J; Abu-Shilbayen L
CORPORATE SOURCE: Univ.America-Cath.
LOCATION: The Catholic University of America, Washington, DC, USA.
SOURCE: Abstr.Gen.Meet.Am.Soc.Microbiol.; (1998) 98 Meet., 237
CODEN: 0005P
ISSN: 0067-2777
98th General Meeting of the American Society for Microbiology, Atlanta, GA, USA, 17-21 May, 1998.
DOCUMENT TYPE: Journal
LANGUAGE: English
AN 99-00537 BIOTECHDS
AB In response to the need for a multicomponent vaccine system, a

phage T4 system for the display of foreign **antigens** is being developed. **Hoc** and **Soc** are 2 proteins which coat the outer surface of the phage T4. Phage T4 was chosen for the system because the high copy number of these proteins allows for the expression of many epitopes on one phage and because these proteins are not essential for phage assembly and infectivity. 2 Plasmid vectors were constructed to allow in-frame fusion of a foreign epitope to the N-terminus of **Hoc** or **Soc**. A 36 **amino** acid PorA peptide from Neisseria meningitidis was used to test the system. The PorA-**Soc** and PorA-**Hoc** fusion proteins were displayed on the T4 **capsid** surface and were highly immunogenic in mice. Strong **antibody** titers were elicited even with a weak adjuvant, like alhydrogel, or no adjuvant at all. Green florescent protein is now also being used as a marker **antigen** for the construction of additional vectors. Eventually, the selection of suitable vectors that would allow stable, high copy number, display of foreign **antigens** for the construction of multicomponent vaccines is hoped to be achieved. (0 ref)

L8 ANSWER 7 OF 27 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
ACCESSION NUMBER: 1997-363387 [33] WPIDS
DOC. NO. NON-CPI: N1997-302145
DOC. NO. CPI: C1997-116417
TITLE: Kaposi's sarcoma associated herpes virus **small** viral **capsid** **antigen** - useful in clinical tests for KS infections and KS associated herpes virus infections.
DERWENT CLASS: B04 D16 P31
INVENTOR(S): GROGAN, E; HESTON, L; LIN, S; MILLER, G; RIGSBY, M; SUN, R
PATENT ASSIGNEE(S): (UYYA) UNIV YALE
COUNTRY COUNT: 21
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9724057	A2	19970710	(199733)*	EN	91
RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: AU CA JP US					
AU 9715219	A	19970728	(199746)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9724057	A2	WO 1996-US20839	19961226
AU 9715219	A	AU 1997-15219	19961226

Searcher : Shears 308-4994

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9715219	A	Based on	WO 9724057

PRIORITY APPLN. INFO: US 1995-9267 19951227
AN 1997-363387 [33] WPIDS
AB WO 9724057 A UPAB: 19970813
The following methods are claimed: (A) diagnosing a DNA virus associated with Kaposi's sarcoma (KS) comprising: (a) contacting a suitable body fluid sample from a patient to a support to which a KS **antibody** (Ab) or **antigen** (Ag) is bound; (b) removing unbound sample from the support, and determining the level of KS Ab or Ag bound by the KS Ag or Ab; and (B) screening for KS-herpes virus (KS-HV) Ab or Ag comprising obtaining a sample from the patient, and assaying for Ab to KS-HV-**small** viral **capsid antigen** (KS-HV-SVCA) or other lytic cycle Ag. An isolated nucleic acid molecule (I) comprises a sequence of a genomic DNA clone or a cDNA encoding KS-HV-SVCA, where the non-coding strand of the DNA or cDNA hybridises under stringent conditions with the DNA probe having the 836 bp nucleic acid sequence given in the specification, or a degenerate or complementary sequence to this, is new. Also claimed are: (1) an expression vector comprising (I); (2) a host cell transformed or transfected with (I); (3) a **polypeptide** encoded by (I); (4) an isolated DNA molecule (II) comprising the 836 bp sequence; (5) an isolated nucleic acid molecule (III) comprising residues 180 to 689 of the 836 bp sequence; (6) a **polypeptide** encoded by (III); and (7) a vector or host cell comprising (II).

USE - The **polypeptide** of (3) can be used in an immunological assay for KS (claimed), while the methods and products can be used in clinical tests for KS infections and KS-HV infections, for diagnosis, to follow therapy and to monitor blood products for transfusion. The methods also provide a serological test for Ab to lytic cycle Ag of KS-HV or HHV8 (human herpes virus 8), and can detect the expression of KS associated lytic cycle Ag, e.g. SVCA, in biological samples.

Dwg.0/18

L8 ANSWER 8 OF 27 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1998013112 MEDLINE
DOCUMENT NUMBER: 98013112
TITLE: Display of a PorA peptide from Neisseria meningitidis on the bacteriophage T4 capsid surface.
AUTHOR: Jiang J; Abu-Shilbayeh L; Rao V B
CORPORATE SOURCE: Department of Biology, The Catholic University of America, Washington, D.C. 20064, USA.

Searcher : Shears 308-4994

SOURCE: INFECTION AND IMMUNITY, (1997 Nov) 65 (11) 4770-7.
Journal code: GO7. ISSN: 0019-9567.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
ENTRY MONTH: 199801
ENTRY WEEK: 19980104

AB The exterior of bacteriophage T4 **capsid** is coated with two outer **capsid** proteins, **Hoc** (**highly** antigenic outer **capsid** protein; molecular mass, 40 kDa) and **Soc** (**small** outer **capsid** protein; molecular mass, 9 kDa), at symmetrical positions on the icosahedron (160 copies of **Hoc** and 960 copies of **Soc** per **capsid** particle). Both these proteins are nonessential for phage infectivity and viability and assemble onto the **capsid** surface after completion of **capsid** assembly. We developed a phage display system which allowed in-frame fusions of foreign DNA at a unique cloning site in the 5' end of **hoc** or **soc**. A DNA fragment corresponding to the 36-**amino** -acid PorA peptide from Neisseria meningitidis was cloned into the display vectors to generate fusions at the N terminus of **Hoc** or **Soc**. The PorA-**Hoc** and PorA-**Soc** fusion proteins retained the ability to bind to the **capsid** surface, and the bound peptide was displayed in an accessible form as shown by its reactivity with specific monoclonal **antibodies** in an **enzyme**-linked immunosorbent assay. By employing T4 genetic strategies, we show that more than one subtype-specific PorA peptide can be displayed on the **capsid** surface and that the peptide can also be displayed on a DNA-free empty **capsid**. Both the PorA-**Hoc** and PorA-**Soc** recombinant phages are highly immunogenic in mice and elicit strong antipeptide **antibody** titers even with a weak adjuvant such as Alhydrogel or no adjuvant at all. The data suggest that the phage T4 **hoc-soc** system is an attractive system for display of peptides on an icosahedral **capsid** surface and may emerge as a powerful system for construction of the next generation multicomponent vaccines.

L8 ANSWER 9 OF 27 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 97213979 MEDLINE
DOCUMENT NUMBER: 97213979
TITLE: Identification, expression, and immunogenicity of Kaposi's sarcoma-associated herpesvirus-encoded **small** viral **capsid antigen**

AUTHOR: Lin S F; Sun R; Heston L; Gradoville L; Shedd D; Haglund K; Rigsby M; Miller G
CORPORATE SOURCE: Department of Molecular Biophysics & Biochemistry,

Yale University School of Medicine, New Haven,
Connecticut 06520, USA.
CONTRACT NUMBER: AI22959 (NIAID)
CA70036 (NCI)
SOURCE: JOURNAL OF VIROLOGY, (1997 Apr) 71 (4) 3069-76.
Journal code: KCV. ISSN: 0022-538X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
OTHER SOURCE: GENBANK-U50141
ENTRY MONTH: 199706
AB We describe a recombinant **antigen** for use in serologic tests for **antibodies** to Kaposi's sarcoma (KS)-associated herpesvirus (KSHV). The cDNA for a **small** viral **capsid antigen** (sVCA) was identified by immunoscreening of a library prepared from the BC-1 body cavity lymphoma cell line induced into KSHV lytic gene expression by sodium butyrate. The cDNA specified a 170-**amino**-acid peptide with homology to **small** viral **capsid** proteins encoded by the BFRF3 gene of Epstein-Barr virus and the ORF65 gene of herpesvirus saimiri. KSHV sVCA was expressed from a 0.85-kb mRNA present late in lytic KSHV replication in BC-1 cells. This transcript was sensitive to phosphonoacetic acid and phosphonoformic acid, inhibitors of herpesvirus DNA replication. KSHV sVCA expressed in mammalian cells or Escherichia coli or translated in vitro was recognized as an **antigen** by antisera from KS patients. Rabbit antisera raised to KSHV sVCA expressed in E. coli detected a 22-kDa protein in KSHV-infected human B cells. Overexpressed KSHV sVCA purified from E. coli and used as an **antigen** in immunoblot screening assay did not cross-react with EBV BFRF3. **Antibodies** to sVCA were present in 89% of 47 human immunodeficiency virus (HIV)-positive patients with KS, in 20% of 54 HIV-positive patients without KS, but in none of 122 other patients including children born to HIV-seropositive mothers and patients with hemophilia, autoimmune disease, or nasopharyngeal carcinoma. Low-titer **antibody** was detected in three sera from 28 healthy subjects. **Antibodies** to recombinant sVCA correlate with KS in high-risk populations. Recombinant sVCA can be used to examine the seroepidemiology of infection with KSHV in the general population.

L8 ANSWER 10 OF 27 MEDLINE
ACCESSION NUMBER: 97314152 MEDLINE
DOCUMENT NUMBER: 97314152
TITLE: Five complete genomes of JC virus type 3 from Africans and African Americans.
AUTHOR: Agostini H T; Ryschkewitsch C F; Brubaker G R; Shao J; Stoner G I

CORPORATE SOURCE: Laboratory of Experimental Neuropathology, National Institute of Neurological Disorders and Stroke, NIH, Bethesda, Maryland, USA.
SOURCE: ARCHIVES OF VIROLOGY, (1997) 142 (4) 637-55.
Journal code: 8L7. ISSN: 0304-8608.
PUB. COUNTRY: Austria
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
OTHER SOURCE: GENBANK-M35834; GENBANK-U73500; GENBANK-U21837; GENBANK-U21838; GENBANK-U21836; GENBANK-U73178; GENBANK-J02227; GENBANK-M20322; GENBANK-U21839; GENBANK-U21840; GENBANK-U21841; GENBANK-U21842; GENBANK-U21843; GENBANK-U21844; GENBANK-M20775; GENBANK-V01108; GENBANK-D13942; GENBANK-X02449; GENBANK-K02449; GENBANK-M57473; GENBANK-J02288; GENBANK-J02400
ENTRY MONTH: 199708
ENTRY WEEK: 19970803

AB The central demyelinating disease progressive multifocal leukoencephalopathy (PML) is caused by the human polyomavirus JC virus (JCV). JCV evolved as geographically based genotypes of which Type 3 is an African variant first characterized in HIV-1 positive patients from Tanzania. This study reports the complete sequence of five JCV Type 3 strains. The entire JCV genome was PCR amplified from urine specimens of three African and two African-American individuals. The African consensus sequence was compared to the Type 1 and Type 2 prototype strains, JCV (Mad-1) and JCV(GS/B), respectively. Type 3 differed in 2.2% of its coding region genome from JCV (Mad-1) and in 1.3% from JCV(GS/B). Within the coding region the sequence variation among the three types was **higher** in the **capsid** protein VP1 and in the regulatory protein large T **antigen** than in the agnoprotein or in VP2/3. Notable Type 3-specific changes were located at sites adjacent to the zinc finger motif and near the major donor and acceptor splice junctions of large T **antigen**. Four of the five urinary Type 3 strains had an unrearranged, archetypal regulatory region. African strain #309 showed a 10-bp deletion at a location similar to that previously described for #307 from Tanzania. The African-American Type 3 strain #312 was closely related to the African consensus sequence. The complete genome of a urinary JCV strain from another African-American male, previously reported as a possible Type 5, showed a sequence difference of only 0.52% from the Tanzanian consensus and has been reclassified as a subtype of Type 3.

L8 ANSWER 11 OF 27 BIOTECHDS COPYRIGHT 1999 DERWENT INFORMATION LTD
ACCESSION NUMBER: 97-12571 BIOTECHDS
TITLE: Cloning of linear DNAs in vivo by overexpressed T4

DNA-ligase: construction of a T4 phage hoc gene display vector;
for recombinant protein expression and surface display in Escherichia coli

AUTHOR: Ren Z J; Baumann R G; *Black L W
CORPORATE SOURCE: Univ.Maryland
LOCATION: Department of Biochemistry and Molecular Biology, University of Maryland School of Medicine, Baltimore, MD 21201-1503, USA.
Email: lblack@umabnet.ab.umd.edu

SOURCE: Gene; (1997) 195, 2, 303-11
CODEN: GENED6
ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English

August. Not a good date priority 4/97

AN 97-12571 BIOTECHDS

AB A method was developed for cloning linear DNAs by overexpressing phage T4 DNA-ligase in vivo, using a recombination-deficient Escherichia coli MM383 carrying a plasmid pRBL vector (5584 bp) with an inducible T4 ligase gene. Plasmid integration allowed standard plasmid isolation after linear DNA transformation. Intramolecular ligation allowed high-efficiency recircularization of cohesive and blunt-end terminated linear plasmid DNAs after transformation. Recombinant plasmids could be constructed in vivo by co-transformation with linearized vector plus insert and intermolecular ligation in ligase-positive strains, to give clones without deletions or rearrangements. In vitro packaged lox site terminated plasmid DNAs from T4 were recircularized in vivo with an efficiency comparable to Cre-recombinase. Surface display of a **capsid**-binding 14-**amino**-acid N-terminal peptide extension derivative of **highly** antigenic outer **capsid** protein was achieved via co-transformation with a linear vector and **hoc** gene polymerase chain reaction product. (20 ref)

L8 ANSWER 12 OF 27 MEDLINE DUPLICATE 5

ACCESSION NUMBER: 97385612 MEDLINE
DOCUMENT NUMBER: 97385612

TITLE: Prevalence of Herpesvirus papio 2 in baboons and identification of immunogenic viral **polypeptides**.

AUTHOR: Eberle R; Black D H; Blewett E L; White G L
CORPORATE SOURCE: Department of Infectious Diseases and Physiology, College of Veterinary Medicine, Oklahoma State University, Stillwater 74078-0359, USA.

CONTRACT NUMBER: RR07849 (NCRR)
SOURCE: LABORATORY ANIMAL SCIENCE, (1997 Jun) 47 (3) 256-62.
Journal code: KYS. ISSN: 0023-6764.
PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199710
ENTRY WEEK: 19971005

AB The prevalence of Herpesvirus papio 2 (HVP2) in several groups of captive and wild-caught baboons was determined by detection of anti-HVP2 **antibodies** in 133 sera of adult baboons. Over 90% of newly imported (wild-caught) adult olive baboons (Papio anubis) from Kenya and chacma baboons (P. ursinus) from South Africa were found to have anti-HVP2 titers. Similarly, approximately 85% of captive breeding colony baboons (P. anubis and P. cynocephalus) were seropositive for HVP2. Infected animals were generally easily identifiable by **enzyme**-linked immunosorbent assay because anti-HVP2 IgG titers in immune animals were usually high (16,000 to 64,000). There was little variation in the relative reactivity patterns of individual HVP2-immune sera when tested against herpes simplex viruses 1 and 2, monkey B virus, H. cercopithecus 2, and HVP2, or against different HVP2 strains. Also, differences were not detected between reactivity of olive and chacma baboon immune sera. Analysis of the **polypeptide** specificity of immune sera by western blot identified four viral **antigens** that were consistent targets of immune sera. These **antigens** were the gB glycoprotein, a pair of unidentified glycoproteins of 80 to 100 kDa, the gD glycoprotein, and a series of **smaller capsid** proteins. Additional viral proteins were variably recognized by individual immune sera. The results of this study indicate that HVP2 is a common infection of baboons; there is little antigenic variation among HVP2 strains; and there are several HVP2 **antigens** that represent consistent targets of the anti-HVP2 immune response of baboons.

L8 ANSWER 13 OF 27 PROMT COPYRIGHT 1999 IAC DUPLICATE 6

ACCESSION NUMBER: 97:264276 PROMT
TITLE: Kaposi's sarcoma (KSHV) "Identification, Expression, and Immunogenicity of Kaposi's sarcoma-Associated Herpesvirus-Encoded **Small** Viral **Capsid Antigen**."
AUTHOR(S): Miller, G.
SOURCE: Cancer Weekly Plus, (12 May 1997) pp. N/A.
LANGUAGE: English
WORD COUNT: 339
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Lin, S.F.; Sun, R.; Heston, L.; Gradoville, L.; Shedd, D.; Haglund, K.; Rigsby, M.; Miller, G.
Journal of Virology, April 1997;71(4):3069-3076.
According to the authors' abstract of an article published in Journal of Virology, "We describe a recombinant **antigen**

for use in serologic tests for **antibodies** to Kaposi's sarcoma (KS)-associated herpesvirus (KSHV). The cDNA for a **small** viral **capsid antigen** (sVCA) was identified by immunoscreening of a library prepared from the BC-1 body cavity lymphoma cell line induced into KSHV lytic gene expression by sodium butyrate. The cDNA specified a 170-**amino**-acid peptide with homology to **small** viral **capsid** proteins encoded by the BFRF3 gene of Epstein-Barr virus and the ORF65 gene of herpesvirus saimiri, KSHV sVCA was expressed from a 0.85-kb mRNA present late in lytic KSHV replication in BC-1 cells. This transcript was sensitive to phosphonoacetic acid and phosphonoformic acid, inhibitors of herpesvirus DNA replication. KSHV sVCA expressed in mammalian cells or Escherichia coli or translated in vitro was recognized as an **antigen** by antisera from KS patients. Rabbit antisera raised to KSHV sVCA expressed in E. coli detected a 22-kDa protein in KSHV-infected human B cells. Overexpressed KSHV sVCA purified from E. coli and used as an **antigen** in immunoblot screening assay did not cross-react with EBV BFRF3. **Antibodies** to sVCA were present in 89% of 47 human immunodeficiency virus (HIV)-positive patients with KS, in 20% of 54 HIV-positive patients without KS, but in none of 122 other patients including children born to HIV-seropositive mothers and patients with hemophilia, autoimmune disease, or nasopharyngeal carcinoma. Low-titer **antibody** was detected in three sera from 28 healthy subjects. **Antibodies** to recombinant sVCA correlate with KS in high-risk populations. Recombinant sVCA can he used to examine the seroepidemiology of infection with KSHV in the general population." The corresponding author for this study is: G Miller, 420 Lsog, 333 Cedar St, New Haven, CT 06520 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L8 ANSWER 14 OF 27 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 97:552376 PROMT
TITLE: Poliovirus: "Poliovirus Sabin Type 1 Neutralization Epitopes Recognized Immunoglobulin A Monoclonal **Antibodies**."
SOURCE: Vaccine Weekly, (6 Oct 1997) pp. N/A.
ISSN: 1074-2921.
LANGUAGE: English
WORD COUNT: 355
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Fiore, L.; Ridolfi, B.; Genovese, D.; Buttinelli, G.; Lucioli, S.; Lahm, A.; Ruggeri, F.M. Journal of Virology, September 1997;71(9):6905-6912.
According to the authors' abstract of an article published in

Journal of Virology, "Immunity to poliomyelitis is largely dependent on humoral neutralizing **antibodies**, both after natural (wild virus or vaccine) infection and after inactivated poliovirus vaccine inoculation. Although the production of local secretory immunoglobulin A (IgA) **antibody** in the gut mucosa may play a major role in protection, most of information about the antigenic determinants involved in neutralization of polioviruses derives from studies conducted with humoral monoclonal **antibodies** (MAbs) generated from parenterally immunized mice. To investigate the specificity of the mucosal immune response to the virus, we have produced a library of IgA MAbs directed at Sabin type 1 poliovirus by oral immunization of mice with live virus in combination with cholera toxin. The epitopes recognized by 13 neutralizing MAbs were characterized by generating neutralization-escape virus mutants. Cross-neutralization analysis of viral mutants with MAbs allowed these epitopes to be divided into four groups of reactivity. To determine the epitope specificity of MAbs, virus variants were sequenced and the mutations responsible for resistance to the **antibodies** were located. Eight neutralizing MAbs were found to be directed at neutralization site N-AgIII in **capsid** protein VP3; four more MAbs recognized site N-AgII in VP1 or VP2. One IgA MAb selected a virus variant which presented a unique mutation at **amino** acid 138 in VP2, not previously described. This site appears to be partially related with site N-AgII and is located in a loop region facing the VP2 N-Ag-II loop ground residue 164. Only 2 of 13 MAbs proved able to neutralize the wild-type Mahoney strain of poliovirus. The IgA **antibodies** studied were found to be produced in the dimeric form needed for recognition by the polyimmunoglobulin **receptor** mediating secretory **antibody** transport at the mucosal level." The corresponding author for this study is: L Fiore, Ist Super Sanita, Virol Lab, Viale Regina Elena 299, I-00161 Rome, Italy. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L8 ANSWER 15 OF 27 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 1998:8847 PROMT
TITLE: Neisseria meningitidis "Display of a PorA Peptide from Neisseria meningitidis on the Bacteriophage T4 Capsid Surface."
SOURCE: Vaccine Weekly, (22 Dec 1997) pp. N/A.
ISSN: 1074-2921.
LANGUAGE: English
WORD COUNT: 340
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Jiang, J.; Abushilbayeh, L.; Rao, V.B. Infection and Immunity,

November 1997;65(11):4770-4777.
According to the authors' abstract of an article published in Infection and Immunity, "The exterior of bacteriophage T4 **capsid** is coated with two outer **capsid** proteins, **Hoc** (**highly** antigenic outer **capsid** protein; molecular mass, 40 kDa) and **Soc** (**small** outer **capsid** protein; molecular mass, 9 kDa), at symmetrical positions on the icosahedron (160 copies of **Hoc** and 960 copies of **Soc** per **capsid** particle). Both these proteins are nonessential for phage infectivity and viability and assemble onto the **capsid** surface after completion of **capsid** assembly. We developed a phage display system which allowed in-frame fusions of foreign DNA at a unique cloning site in the 5' end of **Hoc** or **Soc**. A DNA fragment corresponding to the 36-**amino**-acid PorA peptide from Neisseria meningitidis was cloned into the display vectors to generate fusions at the N terminus of **Hoc** or Sec. The PorA-**Hoc** and PorA-**Soc** fusion proteins retainedthe ability to bind to the **capsid** surface, and the bound peptide was displayed in an accessible form as shown by its reactivity with specific monoclonal **antibodies** in an **enzyme**-linked immunosorbent assay. By employing T4 genetic strategies, we show that more than one subtype-specific PorA peptide can be displayed on the **capsid** surface and that the peptide can also be displayed on a DNA-free empty **capsid**. Both the PorA-**Hoc** and PorA-**Soc** recombinant phages are highly immunogenic in mice and elicit strong antipeptide **antibody** titers even with a weak adjuvant such as Alhydrogel or no adjuvant at all. The data suggest that the phage T4 **hoc-soc** system is an attractive system for display of peptides on an icosahedral **capsid** surface and may emerge as a powerful system for construction of the next generation multicomponent vaccines." The corresponding author for this study is: VB Rao, Catholic Univ Amer, Dept Biol, 103 Mccort Ward Hall, 620 Michigan Ave NE, Washington, DC 20064 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L8 ANSWER 16 OF 27 MEDLINE
ACCESSION NUMBER: 96183616 MEDLINE
DOCUMENT NUMBER: 96183616
TITLE: Immune response to epitopes of hepatitis C virus (HCV) structural proteins in HCV-infected humans and chimpanzees.
AUTHOR: Wang Y F; Brotman B; Andrus L; Prince A M
CORPORATE SOURCE: Laboratory of Virology and Parasitology, New York Blood Center, New York City, USA.

CONTRACT NUMBER: HE-09011
SOURCE: JOURNAL OF INFECTIOUS DISEASES, (1996 Apr) 173 (4) 808-21.
Journal code: IH3. ISSN: 0022-1899.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199607

AB Hepatitis C virus (HCV)-infected humans and chimpanzees were studied for reactivity with linear epitopes in HCV H strain structural proteins. In 10 HCV-infected patients, epitopes were mostly mapped to the capsid and E1 proteins but not to E2. However, serum from 1 HCV-infected blood donor with a **high** anti-**capsid** titer reacted with multiple epitopes including E2. By contrast, **antibody** to capsid epitopes was seen in sera from HCV-rechallenged chimpanzees but not from chronically infected animals. No reactivity was observed to GOR epitope in chimpanzees, while 6 of 11 human subjects reacted with this host-coded **antigen**. Reactivity to rare epitopes in E2 was seen in chimpanzees with chronic and self-limited infections. Reactivity to one peptide of E1 (aa 316-329) was observed in 10 of 11 sera from HCV-infected humans and 11 of 15 chimpanzee sera. However, reactivity to this epitope was also seen in normal chimpanzees and in 6 (7.1%) of 84 uninfected human subjects.

L8 ANSWER 17 OF 27 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 96:86745 PROMT
TITLE: Dengue Virus Gagnon, S.J.; Zeng, W.L.; Kurane, I.; Ennis, F.A. "Identification of Two Epitopes on the Dengue 4 Virus Capsid Protein Recognized by a Serotype-Specific and a Panel of Serotype-Cross-Reactive Human CD4(+) Cytotoxic T-Lymphocyte Clones." Journal of Virology, January 1996;70(1):141-147.
SOURCE: Vaccine Weekly, (29 Jan 1996) pp. N/A.
ISSN: 1074-2921.
LANGUAGE: English
WORD COUNT: 395
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB According to the authors' abstract of an article published in Journal of Virology, "We analyzed the CD4(+) T-lymphocyte response of a donor who had received an experimental live-attenuated dengue 4 virus (D4V) vaccine. Bulk culture proliferative responses of peripheral blood mononuclear cells (PBMC) to noninfectious dengue virus (DV) **antigens** showed the highest proliferation to D-IV **antigen**, with lesser, cross reactive proliferation to D2V **antigen**. We established CD4(+) cytotoxic T-lymphocyte clones (CTL) by stimulation with D4 **antigen**. Using

recombinant baculovirus **antigens**, we identified seven CTL clones that recognized D4V capsid protein. Six of these CTL clones were cross-reactive between D2 and D4, and one clone was specific for D4. Using synthetic peptides. we found that the D4V-specific CTL clone recognized an epitope between **amino** acids (aa) 47 and 55 of the capsid protein, while the cross-reactive CTL clones each recognized epitopes in a separate location, between aa 83 and92, which is conserved between D2V and D4V. This region of the capsid protein induced a variety of CD4 T-cell responses, as indicated by the fact that six clones which recognized a peptide spanning this region shelved heterogeneity in their recognition of truncations of this same peptide. The bulk culture response of the donor's PBMC to the epitope peptide spanning aa 81 to 92 was also examined. Peptides containing this epitope induced proliferation of the donor's PBMC in bulk culture, but peptides not containing the entire epitope did not induce proliferation. Also, PBMC stimulated in bulk culture with noninfectious D4V **antigen** lysed autologous target cells pulsed with peptides containing aa 84 to 92. These results indicate that this donor exhibits memory CD4(+) T-cell responses directed against the DV capsid protein and suggest that the response to the capsid protein is dominant not only in vitro at the clonal level but in bulk culture responses as well. Since previous studies have indicated that the CTL responses to DV infection seem to be directed mainly against the envelope (E) and NS3 proteins, these results are the first to indicate that the DV capsid protein is also a target of the antiviral T-cell response." The corresponding author for this study is: FA Ennis, Univ Massachusetts, Med Ctr, Dept Med, Div Infect Dis & Immunol, 55 Lake Ave N, Worcester, MA 01655 USA.

L8 ANSWER 18 OF 27 MEDLINE DUPLICATE 7

ACCESSION NUMBER:	96263876 MEDLINE
DOCUMENT NUMBER:	96263876
TITLE:	Assembly and antigenicity of hepatitis B virus core particles.
AUTHOR:	Seifer M; Standring D N
CORPORATE SOURCE:	Hormone Research Institute, University of California at San Francisco, USA.
CONTRACT NUMBER:	A12506
SOURCE:	INTERVIROLOGY, (1995) 38 (1-2) 47-62. Ref: 61 Journal code: GW7. ISSN: 0300-5526.
PUB. COUNTRY:	Switzerland Journal; Article; (JOURNAL ARTICLE) General Review; (REVIEW) (REVIEW, TUTORIAL)
LANGUAGE:	English
FILE SEGMENT:	Priority Journals
ENTRY MONTH:	199610

AB Recent studies in Xenopus oocytes and other systems have led to an understanding of the HBV capsid, or core particle, assembly process. Nascent HBV core **polypeptides** rapidly dimerize. Accumulation of free dimers to a signature concentration (approximately 0.8 microM) then triggers a **highly** cooperative **capsid** assembly reaction. This dimer-to-capsid transition is accompanied by a switch from HBe to HBc antigenicity and appears to be nucleated by interaction between core protein and RNA: deletion of a protamine-like RNA binding domain at the C-terminus of the core protein markedly increases the concentration of dimers needed to drive capsid assembly. The simple assembly pathway seen for HBV capsids mirrors that of R17 bacteriophage.

L8 ANSWER 19 OF 27 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 95:464329 PROMT
TITLE: HCV Vaccines Major, M.E.; Vitvitski, L.; Mink, M.A.; Schleef, M.; Whalen, R.G.; Trepo, C.; Inchauspe, G. "DNA-Based Immunization with Chimeric Vectors for the Induction of Immune Responses Against the Hepatitis C Virus Nucleocapsid." Journal of Virology, September 1995;69(9):5798-5805.
SOURCE: Vaccine Weekly, (25 Sep 1995) pp. N/A.
ISSN: 1074-2921.
LANGUAGE: English
WORD COUNT: 263
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB According to the authors' abstract of an article published in Journal of Virology, "Vectors expressing the first 58 **amino** acids of the hepatitis C virus (HCV) nucleocapsid alone or as a fusion protein with the middle (pre-S2 and S) or major (S) surface **antigens** of hepatitis B virus (HBV) were constructed. Intramuscular immunization of BALB/c mice with the chimeric constructs in the form of naked DNA elicited humoral responses to **antigens** from both viruses within 2 to 6 weeks postinjection. No anti-HCV responses were obtained in mice immunized with the vector expressing the HCV sequence in the nonfusion context. Sera from chimera-injected mice specifically recognized both HCV **capsid** and HBV surface **antigens** in **enzyme**-linked immunosorbent assay and immunoblot testing. Anti-HCV serum titers formed plateaus of approximately 1:3,000; these remained stable until the end of the study (18 weeks postinfection). Anti-HBV immune responses were found to be lower in the chimera-injected animals (less than 200 mIU/ml) than in those immunized with the native HBV vector (greater than 2,000 mIU/ml). This is the first report of the use of DNA-based immunization for the generation of immune responses to an HCV protein. In addition, these findings show that it is possible to elicit responses to viral epitopes from two distinct viruses via DNA immunization with

chimeric vectors." The corresponding author for this study is: G Inchauspe, Sida & Retrovirus Humains, Unite Rech Hepatites, Inserm, U271, 151 Cours Albert Thomas, F-69424 Lyon, France. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.
THIS IS THE FULL TEXT: COPYRIGHT 1995 Charles W Henderson

L8 ANSWER 20 OF 27 BIOTECHDS COPYRIGHT 1999 DERWENT INFORMATION LTD
ACCESSION NUMBER: 93-00777 BIOTECHDS
TITLE: Recombinant protein production in Escherichia coli using vector plasmid pFRHIV 12-50; phage fr coat protein and HIV virus env protein recombinant fusion protein preparation; potential as recombinant vaccine
PATENT ASSIGNEE: Humboldt-Univ.Berlin
PATENT INFO: DD 300652 25 Jun 1992
APPLICATION INFO: DD 90-338995 23 Mar 1990
PRIORITY INFO: DD 90-338995 23 Mar 1990
DOCUMENT TYPE: Patent
LANGUAGE: German
OTHER SOURCE: WPI: 92-382866 [47]
AN 93-00777 BIOTECHDS
AB A process is claimed for the production of a recombinant protein, frCP-HIVenv(474-479) (I), having both HIV virus and phage fr antigenic characteristics, by inserting part of the HIV envelope protein (**amino** acids (AA) 474-759) into the second AA of the coat protein of phage fr. Under preferred conditions, recombinant plasmid pFRHIV-12-50 containing (i) 5279 bp of plasmid pFR771 (containing the ampicillin-resistance gene and the complete fr coat protein gene under a trp promoter), and (ii) 854 bp of HIV virus-1 gene (including the nucleotides between restriction sites BglII(7198) and BamHI(8052) to include the 45 C-terminal AAs of gp120 and 241 N-terminal AAs of gp41) is used for the transformation of Escherichia coli K802, resulting in the producer strain (WKPM W-5239, UdSSR) for (I). Using the recombinant plasmid in E. coli results in the production of phage fr capsids, similar to the original capsids, which are **highly** immunogenic. The **capsids** can easily be isolated by sera against forms of the fr coat protein to yield **antigen** derivatives i.e. of gp41. (6pp)

L8 ANSWER 21 OF 27 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 92085429 MEDLINE
DOCUMENT NUMBER: 92085429
TITLE: The unique sequence of the herpes simplex virus 1 L component contains an additional translated open reading frame designated UL49.5.
AUTHOR: Barker D E; Roizman B

CORPORATE SOURCE: Marjorie B. Kovler Viral Oncology Laboratories, University of Chicago, Illinois 60637..
CONTRACT NUMBER: CA47451 (NCI)
AI24009 (NIAID)
AI1588 (NIAID)
SOURCE: JOURNAL OF VIROLOGY, (1992 Jan) 66 (1) 562-6.
Journal code: KCV. ISSN: 0022-538X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
ENTRY MONTH: 199203
AB We present evidence for the existence of an additional herpes simplex virus 1 gene designated UL49.5. The sequence, located between genes UL49 and UL50, predicts a hydrophobic protein with 91 **amino** acids. Attempts to delete UL49.5 were not successful. To demonstrate that UL49.5 is expressed, we made two recombinant viruses. First, we inserted in frame an oligonucleotide encoding a 15-**amino**-acid epitope known to react with a monoclonal **antibody**. This gene, consisting of the authentic promoter and chimeric coding domain, was inserted into the thymidine kinase gene of wild-type virus and in infected cells expressed a protein which reacted with the monoclonal **antibody**. The second recombinant virus contained a 5' UL49.5-thymidine kinase fusion gene. The protein expressed by this virus confirmed that the first methionine codon of UL49.5 served as the initiating codon. The predicted **amino** acid sequence of UL49.5 is consistent with the known properties of NC-7, a **small capsid** protein whose gene has not been previously mapped. A homolog of UL49.5 is present in the genome of varicella-zoster virus, located between homologs of UL49 and UL50.

L8 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 1999 DERWENT INFORMATION LTD
ACCESSION NUMBER: 91-09803 BIOTECHDS
TITLE: Identification of an immunodominant epitope within the capsid protein of hepatitis C virus; expressed as a fusion protein with glutathione-transferase; potential use in blood screening, diagnosis of hepatitis C virus infection
AUTHOR: Nasoff M S; Zebedee S L; Inchauspe G; *Prince A M
CORPORATE SOURCE: Pharmacia-Genet.Eng.
LOCATION: Pharmacia Genetic Engineering, Inc., La Jolla, CA 92037, USA.
SOURCE: Proc.Natl.Acad.Sci.U.S.A.; (1991) 88, 12, 5462-66
CODEN: PNASA6
DOCUMENT TYPE: Journal
LANGUAGE: English
AN 91-09803 BIOTECHDS
AB cDNA clones were isolated from the 5' end of hepatitis C virus

(HCV) Hutchinson strain. 3 Target sequences derived from the putative capsid region were amplified after 2 rounds of the polymerase chain reaction. Glutathione-S-transferase (GST, EC-2.5.1.18)-capsid fusions were constructed by inserting contiguous segments of the capsid gene into the GST fusion vector plasmid pGEX-3X. To further delineate the location of seroreactive epitopes within the capsid protein, 3 **smaller** GST-**capsid** fusions were constructed by inserting sets of synthetic oligonucleotides encoding 20 **amino** acid proteins into the GST fusion vector plasmid pGEX-2T. The various fusion proteins were expressed in Escherichia coli W3110 and total cell lysates were analyzed by SDS-PAGE. Expression of the capsid fusion proteins varied from 17% to 31% of total cell protein. An immunodominant epitope was located within the N-terminal portion of capsid that was preferentially recognized by **antibodies** in both human and chimpanzee HCV-positive sera. These fusion proteins may be of use in the development of specific tests for blood screening and clinical diagnosis of HCV. (20 ref)

L8 ANSWER 23 OF 27 BIOSIS COPYRIGHT 1999 BIOSIS DUPLICATE 9
ACCESSION NUMBER: 1988:140084 BIOSIS
DOCUMENT NUMBER: BA85:74911
TITLE: ISOLATION AND ANTIGENIC CHARACTERIZATION OF DENSE PARTICLES OF SWINE ENTEROVIRUSES.
AUTHOR(S): URAKAWA T; HAMADA N; SHINGU M
CORPORATE SOURCE: DEP. VIROL., KURUME UNIV. SCH. MED., KURUME, 830 JPN.
SOURCE: KURUME MED J, (1987) 34 (2), 65-74.
CODEN: KRMJAC. ISSN: 0023-5679.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Dense particles (buoyant density in CsCl: 1.45-1.47 g/cm3) were isolated from HeLa cells infected with swine enteroviruses and coxsackievirus type B5. These dense particles had important properties which were different from those of poliovirus and other picornaviruses described previously; for instance, they could be isolated under various conditions of virus growth. The **smallest capsid polypeptide**, VP4, was not detected by SDS-PAGE analysis. The preparations of dense particels were non-infectious and showed H antigenicity by a modified **enzyme** immunoassay. Judging from these properties, dense particles might be equivalent to "A particles". These findings suggest that the VP4 **polypeptide** is responsible for the conformational stabilization of the intact virion.

L8 ANSWER 24 OF 27 MEDLINE
ACCESSION NUMBER: 85126881 MEDLINE
DOCUMENT NUMBER: 85126881
TITLE: Regulation of a new bacteriophage T4 gene, 69, that

spans an origin of DNA replication.
AUTHOR: Macdonald P M; Mosig G
CONTRACT NUMBER: GM 13221 (NIGMS)
RR07201 (NCRR)
T32 GM07319 (NIGMS)
SOURCE: EMBO JOURNAL, (1984 Dec 1) 3 (12) 2863-71.
Journal code: EMB. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-K03113
ENTRY MONTH: 198506
AB We have determined the DNA sequence and transcription patterns in a 3-kb segment (between 15 and 18 kb on the standard phage T4 map) spanning an origin of DNA replication. A new gene, 69, spans this origin. Gene 69 codes for two overlapping proteins that share a common C-terminal segment. Defective DNA replication in an appropriate amber mutant shows that at least the larger of the two proteins is required for efficient T4 DNA replication. The two proteins coded by gene 69 are expressed from different transcripts that are under different regulation. The smaller protein, gp69*, can be expressed immediately from an Escherichia coli-like promoter, whereas expression of the larger protein, gp69, must be delayed since its middle promoter requires T4 coded proteins, most likely gp mot, for activation. We discuss the possible significance of two overlapping proteins in the assembly of replisomes. Gene 69 is bracketed by the non-essential early gene dam (DNA adenine methylase) and the late gene **soc** (**small** outer **capsid** protein). Transcripts through this region are interdigitated in a complex pattern, which reveals all elements that are thought to be important in regulation of pre-replicative and post-replicative T4 genes.

L8 ANSWER 25 OF 27 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 84266136 MEDLINE
DOCUMENT NUMBER: 84266136
TITLE: Interaction of reovirus with cell surface **receptors**. IV. The reovirus type 3 **receptor** is expressed predominantly on murine Lyt-2,3+ and human T8+ cells.
AUTHOR: Epstein R L; Finberg R; Powers M L; Weiner H L
CONTRACT NUMBER: NSAI-16998
NIAID-16701
SOURCE: JOURNAL OF IMMUNOLOGY, (1984 Sep) 133 (3) 1614-7.
Journal code: IFB. ISSN: 0022-1767.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals; Cancer Journals
ENTRY MONTH: 198411
AB Reovirus type 3 binds to approximately 20% of murine and human T cells via the viral hemagglutinin, a **small** outer **capsid polypeptide**. By using purified viral particles as a **ligand** in a standard plate separation technique, we have been able to enrich human peripheral blood and murine splenic T cells for reovirus **receptor**-positive cells (reovirus 3+) to levels of 88 to 92%. Analysis of reovirus 3+ T cells with monoclonal **antibodies** that identify inducer and suppressor/cytotoxic cells demonstrated that in the mouse, 68% of reovirus 3+ cells were Lyt-2+, and in the human, 60% were T8+. In reciprocal experiments, when subpopulations of murine and human T cells were prepared with the use of monoclonal anti-T cell reagents, 16% of Lyt-1+ and 81% of Lyt-2+ cells bound reovirus, whereas 30% of T4+ and 65% of T8+ cells bound reovirus. To determine whether reovirus type 3 identified a functional as well as a phenotypic category of cells, an **antigen**-specific cytotoxic T cell assay was employed. There was complete loss of cytotoxic activity in the reovirus 3+ cell population and slight enhancement of cytotoxic activity in the cell population from which reovirus 3+ cells were removed. This suggested that reovirus was binding to functionally active suppressor cells. Furthermore, adoptive transfer of **antigen**-specific T cells that were enriched for reovirus 3+ cells demonstrated suppression of cytoxic T cell activity. These results suggest that reovirus type 3 may identify a structure common to a subclass of murine and human T cells and that by using the virus as a natural biologic probe for cell surface **receptors**, one may be able to functionally segregate murine cytotoxic from suppressor T cells.

L8 ANSWER 26 OF 27 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 82032271 MEDLINE
DOCUMENT NUMBER: 82032271
TITLE: Antigenic and structural relatedness among non-capsid and capsid **polypeptides** of polioviruses belonging to different serotypes.
AUTHOR: Romanova L I; Tolskaya E A; Agol V I
SOURCE: JOURNAL OF GENERAL VIROLOGY, (1981 Feb) 52 (Pt 2) 279-89.
Journal code: I9B. ISSN: 0022-1317.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198202
AB **Antibodies** were raised by immunization of Macaca fascicularis monkeys with extracts of M. fascicularis kidney cells

separately infected with one of the three poliovirus serotypes. Preparations of **antibodies** were shown to be strictly type-specific in the neutralization test but formed immune complexes adsorbable on Staphylococcus aureus, Cowan I strain cells, with heterotypic as well as homotypic virus-specific **polypeptides** present in extracts from the virus-infected cells. The presence of intertypic antigenic determinants was demonstrated by this technique on both the non-capsid and capsid poliovirus **polypeptides**. Structural variations of poliovirus **polypeptides** were studied by analysing products of their partial proteolysis. Non-capsid **polypeptides** encoded in the central portion of the virus genome (**polypeptides** 5b and X) as well as in the 3'-terminal region (NCVP2 and NCVP4) were found to be **highly** conserved, whereas **capsid polypeptides** VP1, VP2, and VP3, which are encoded in the 5'-terminal region of the virus RNA, displayed a much greater variability.

L8 ANSWER 27 OF 27 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 77144062 MEDLINE
DOCUMENT NUMBER: 77144062
TITLE: The two dispensable structural proteins (**soc** and **hoc**) of the T4 phage **capsid**; their purification and properties, isolation and characterization of the defective mutants, and their binding with the defective heads in vitro.
AUTHOR: Ishii T; Yanagida M
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1977 Feb 5) 109 (4) 487-514.
Journal code: J6V. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197707

(FILE 'CAPLUS' ENTERED AT 16:09:56 ON 02 AUG 1999)
L9 20 S (HOC OR SOC)(S)CAPSID
L10 11 S (HIGH? OR SMALL)(2W)(OUTER CAPSID)
L11 20 S L9 OR L10
L12 17 S L11 NOT L6

=> d 1-17 .bevstr1

L12 ANSWER 1 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1999:28344 CAPLUS
DOCUMENT NUMBER: 130:233061
TITLE: Several new bacteriophage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (a DNA-dependent

ATPase-helicase) modulate transcription

AUTHOR(S): Mosig, Gisela; Colowick, Nancy E.; Pietz, Bradley C.

CORPORATE SOURCE: Department of Molecular Biology, Vanderbilt University, Nasville, TN, 37235, USA

SOURCE: Gene (1998), 223(1-2), 143-155
CODEN: GENED6; ISSN: 0378-1119

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We have analyzed DNA of wild-type T4 and of 13 independent large viable deletions isolated by Homyk and Weil (Virol. 61 (1974) 505-523) and by Little (Virol. 53 (1973) 47-59), by sequencing, cloning, and expression studies. The deletions can be explained by illegitimate recombination between short (4- to 15-bp) ectopic repeats. In four deletions, adjacent regions are partially homologous, and in at least one of them, the base adjacent to the overlap was deleted during recombination. The sequence 5'-GGGC, which has not been assocd. with T4 deletions in other map regions, occurs within three repeats, and near the repeats in four more of the 13 deletions. Five previously named genes, 69, soc, mrh, modA, and dda were mapped relative to the deletion endpoints. Nine addnl. ORFs were found interspersed between them. One of these shares some similarities with mrh (modulates rpoH; Frazier and Mosig, Gene 88 (1990) 7-14), and another one resembles modA (coding for an ADP-ribosyl-transferase that modifies RNA polymerase .alpha. subunits, Skorko et al., Eur. J. Biochem. 79 (1977) 55-66) resp. We found that the host's heat shock sigma factor, .sigma.32, is phosphorylated, and that Mrh protein modulates this phosphorylation. The ORF dda.9 downstream of mrh has a patchy similarity with conserved C-terminal segments (motifs) of .sigma.32; therefore, we call it srh. Another ORF, dda.2 located between modA and dda, shares sequence similarity with .sigma.70, and we call it srd. We consider the possibility that Srh and Srd act as decoys for .sigma.32, or .sigma.70, resp. Expression of several of the ORFs from cloned DNA appears to be toxic to the host bacteria. Mutant clones only could be constructed from gene 69 and from modA. Moreover, dda.2 (srd)-contg. bacteria grow extremely slowly, and they form filaments in liq. cultures. Clones carrying mrh and srh show less severe filamentation. Our results highlight the importance of 'non-essential' genes for phage development and evolution.

IT Genes (microbial)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(56; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)

IT Genes (microbial)
RL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)
(69; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)
IT Phosphorylation (biological)
(coliphage T4 Mrh protein modulates phosphorylation of host sigma factor .sigma.32)
IT .sigma.-70 Factor (transcription factor)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(coliphage T4 gene products Srh and Srd as decoys for .sigma.32 or .sigma.70, resp.)
IT Coliphage T4
DNA sequences
Genetic mapping
Protein sequences
Transcriptional regulation
(coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)
IT Genes (microbial)
RL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)
(dda; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)
IT DNA helicases
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gene dda; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)
IT **Capsid** proteins
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(gene **soc (small outer capsid)**; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)
IT Proteins (specific proteins and subclasses)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene srd; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)
IT Proteins (specific proteins and subclasses)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(gene srh; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)

IT Genes (microbial)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(modA; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)

IT Genes (microbial)
RL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)
(mrh.1 (modulates rpoH); coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)

IT Genes (microbial)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(mrh.2 (modulates rpoH); coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)

IT Genes (microbial)
RL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)
(**soc (small outer capsid**); coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)

IT Genes (microbial)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(srd (similar to rpoD); coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)

IT Genes (microbial)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(srh (similar to rpoH); coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)

IT .sigma. Factor (transcription factor)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(.sigma.-32, gene rpoH; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda

(DNA-dependent ATPase-helicase), modulate transcription)
IT 129288-93-3, Protein (coliphage T4 clone pMFs37 gene soc.-1)
197181-80-9, (Adenosine diphosphoribose)transferase, nicotinamide adenine dinucleotide-protein (coliphage T4 gene modA) 197181-81-0, (Adenosine diphosphoribose)transferase, nicotinamide adenine dinucleotide-protein (coliphage T4 gene modB) 213671-78-4
213671-79-5, Protein (bacteriophage T4 gene soc N-terminal fragment)
221269-93-8 221269-94-9 221269-95-0 221269-96-1 221269-97-2
221313-92-4 221313-96-8 221313-98-0
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)
IT 9024-87-7, Deoxycytidine triphosphatase 58319-92-9, ADP-ribosyltransferase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)
IT 9014-24-8, Rna polymerase
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(gene rpoH; coliphage T4 Mrh protein modulates phosphorylation of host sigma factor .sigma.32)
IT 140266-54-2, GenBank M30001
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; coliphage T4 genes, mapped by sequencing deletion endpoints between genes 56 (dCTPase) and dda (DNA-dependent ATPase-helicase), modulate transcription)

L12 ANSWER 2 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1997:504777 CAPLUS
DOCUMENT NUMBER: 127:215644
TITLE: Cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.
AUTHOR(S): Ren, Z. J.; Baumann, R. G.; Black, L. W.
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Maryland School of Medicine, Baltimore, USA
SOURCE: Gene (1997), 195(2), 303-311
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A method was developed to clone linear DNAs by overexpressing T4 phage DNA ligase in vivo, based upon recombination deficient E. coli derivs. that carry a plasmid contg. an inducible T4 DNA ligase gene. Integration of this ligase-plasmid into the chromosome of such E. coli allows std. plasmid isolation following linear DNA transformation of the strains contg. high levels of T4 DNA ligase. Intramol. ligation allows high efficiency recircularization of cohesive and blunt-end terminated linear plasmid DNAs following transformation. Recombinant plasmids could be constructed in vivo by co-transformation with linearized vector plus insert DNAs, followed by intermol. ligation in the T4 ligase strains to yield clones without deletions or rearrangements. Thus, in vitro packaged lox-site terminated plasmid DNAs injected from phage T4 were recircularized by T4 ligase in vivo with an efficiency comparable to CRE recombinase. Clones that expressed a **capsid**-binding 14-aa N-terminal peptide extension deriv. of the **HOC** (**highly** antigenic **outer capsid**) protein for T4 phage **hoc** gene display were constructed by co-transformation with a linearized vector and a PCR-synthesized **hoc** gene. Therefore, the T4 DNA ligase strains are useful for cloning linear DNAs in vivo by transformation or transduction of DNAs with nonsequence-specific but compatible DNA ends.

IT Genetic vectors
(T4 phage; cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.)

IT Coliphage T4
Molecular cloning
(cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.)

IT Genes (microbial)
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(hoc; clones expressing HOC protein for T4 phage hoc gene display were constructed by co-transformation with a linearized vector and a PCR-synthesized hoc gene)

IT Plasmids
(intramol. ligation allows high efficiency recircularization of cohesive and blunt-end linear plasmid DNAs; cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.)

IT Circular DNA
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(intramol. ligation allows high efficiency recircularization of cohesive and blunt-end linear plasmid DNAs; cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.)

IT DNA
RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation); PROC (Process)
(linear; cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.)
IT Genes (microbial)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(lox, in vitro packaged lox-site terminated plasmid DNAs injected from phage T4 were recircularized by T4 ligase; cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.)
IT Gene expression
(over-; cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.)
IT 9015-85-4P, DNA ligase
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(T4; cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.)

L12 ANSWER 3 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1997:454435 CAPLUS
DOCUMENT NUMBER: 127:189413
TITLE: A member of the immunoglobulin superfamily in bacteriophage T4
AUTHOR(S): Bateman, Alex; Eddy, Sean R.; Mesyanzhinov, Vadim V.
CORPORATE SOURCE: MRC Laboratory Molecular Biology, Cambridge, CB2 2QH, UK
SOURCE: Virus Genes (1997), 14(2), 163-165
CODEN: VIGEET; ISSN: 0920-8569
PUBLISHER: Kluwer
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors report a prediction that the **highly** immunogenic **outer capsid** (**Hoc**) protein of the prokaryotic phage T4 contains three tandem Ig-like domains. Ig-like folds have previously been identified in prokaryotic proteins but these share no recognizable sequence similarity with eukaryotic Ig superfamily (IgSF) folds, and may represent products of convergent evolution. In contrast, the Hoc Ig-like folds are proposed, based on Ig-like sequence consensus matches detected by hidden Markov modeling. The authors propose that the Hoc Ig-like domains and eukaryotic Ig-like domains are likely to be related by divergence from a common ancestor.
IT **Capsid** proteins

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(**Hoc**; member of Ig superfamily in bacteriophage T4)
IT Biological simulation
(Markov; member of Ig superfamily in bacteriophage T4)
IT Coliphage T4
Molecular evolution
Prokaryote
(member of Ig superfamily in bacteriophage T4)
IT Ig-like domain
Repeat motifs (protein)
(three tandem IgSF domains; member of Ig superfamily in bacteriophage T4)

L12 ANSWER 4 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1996:572778 CAPLUS
DOCUMENT NUMBER: 125:266696
TITLE: Phage display of intact domains at high copy number: a system based on **SOC**, the **small outer capsid** protein of bacteriophage T4
AUTHOR(S): Ren, Z. J.; Lewis, G. K.; Wingfield, P. T.; Locke, E. G.; Steven, A. C.; Black, L. W.
CORPORATE SOURCE: Department of Biological Chemistry, University of Maryland School of Medicine, Baltimore, MD, 21201, USA
SOURCE: Protein Sci. (1996), 5(9), 1833-1843
CODEN: PRCIEI; ISSN: 0961-8368
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Peptides fused to the coat proteins of filamentous phages have found widespread applications in antigen display, the construction of antibody libraries, and biopanning. However, such systems are limited in terms of the size and no. of the peptides that may be incorporated without compromising the fusion proteins' capacity to self-assemble. We describe here a system in which the mols. to be displayed are bound to pre-assembled polymers. The polymers are T4 **capsids** and polyheads (tubular **capsid** variants) and the display mols. are derivs. of the dispensable **capsid** protein **SOC**. In one implementation, SOC and its fusion derivs. are expressed at high levels in Escherichia coli, purified in high yield, and then bound in vitro to sep. isolated polyheads. In the other, a pos. selection vector forces integration of the modified soc gene into a soc-deleted T4 genome, leading to in vivo binding of the display protein to progeny virions. The system is demonstrated as applied to C-terminal fusions to **SOC** of (1) a tetrapeptide (Cys-Leu-Asn-Ser); (2) the 43-residue V3 loop domain of gp 120, the human immunodeficiency virus type-1 (HIV-1) envelope glycoprotein; and (3) poliovirus VP1 **capsid**

protein (312 residues). SOC-V3 displaying phage were highly antigenic in mice and produced antibodies reactive with native gp 120. That the fusion protein binds correctly to the surface lattice was attested in averaged electron micrographs of polyheads. The **SOC** display system is capable of presenting up to .apprx.103 copies per **capsid** and >104 copies per polyhead of V3-sized domains. Phage displaying SOC-VP1 were isolated from a 1:106 mixt. by two cycles of a simple biopanning procedure, indicating that proteins of at lease 35 kDa may be accommodated.

IT Plasmid and Episome
(pRH, integration vector; use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT Combinatorial library
(peptide and protein, methodol.; use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT Genetic methods
(phage display; use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT Peptides, preparation
Proteins, specific or class, preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(phage display; use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT Virus, bacterial
(T4, use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(VP1, fusion products, with **SOC** protein; use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(gene **soc**, fusion products, with peptides or proteins; use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT Proteins, specific or class
RL: BUU (Biological use, unclassified); BIOL (Biological study);

USES (Uses)
(gene **soc**, scaffold; use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT Sialoglycoproteins
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(gp120env, fusion products, with **SOC** protein; use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT Gene, microbial
RL: BPR (Biological process); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)
(**soc**, use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

IT 182356-70-3DP, fusion products, with **SOC** protein
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(use of **SOC**, the **small outer capsid** protein of bacteriophage T4, as a scaffold for phage display of peptides and proteins)

L12 ANSWER 5 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1993:54666 CAPLUS
DOCUMENT NUMBER: 118:54666
TITLE: Conformational changes of a viral **capsid** protein. Thermodynamic rationale for proteolytic regulation of bacteriophage T4 **capsid** expansion, cooperativity, and super-stabilization by **Soc** binding
AUTHOR(S): Steven, Alasdair C.; Greenstone, Heather L.; Booy, Frank P.; Black, Lindsay W.; Ross, Philip D.
CORPORATE SOURCE: Lab. Struct. Biol., Natl. Inst. Arthritis Musculoskeletal Skin Dis., Bethesda, MD, 20892, USA
SOURCE: J. Mol. Biol. (1992), 228(3), 870-84
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Differential scanning calorimetry was used in conjunction with cryo-electron microscopy to investigate the conformational transitions undergone by the maturing capsid of phage T4. Its precursor shell is composed primarily of gp23 (521 residues): cleavage of gp23 to gp23* (residues 66 to 521) facilitates a concerted conformational change in which the particle expands

substantially, and is greatly stabilized. The intermediate states of capsid maturation have now been characterized; namely, the cleaved/unexpanded, state, which denatures at tm = 60.degree., and the uncleaved/expanded state, for which tm = 70.degree.. When compared with the precursor uncleaved/unexpanded state (tm = 65.degree.), and the mature cleaved/expanded state (tm = 83.degree., if complete cleavage precedes expansion), it follows that expansion of the cleaved precursor (.DELTA.tm .apprx. +23.degree.) is the major stabilizing event in capsid maturation. These observations also suggest an advantage conferred by capsid protein cleavage (some other phage capsids expand without cleavage): if the gp23.DELTA. domains (residues 1 to 65) are not removed by proteolysis, they impede formation of the stablest possible bonding arrangement when expansion occurs, most likely by becoming trapped at the interface between neighboring subunits or capsomers. Icosahedral capsids denature at essentially the same temps. as tubular polymorphic variants (polyheads) for the same state of the surface lattice. However, the thermal transitions of capsids are considerably sharper, i.e. more co-operative, than those of polyheads, which we attribute to capsids being closed, not open-ended. In both cases, binding of the accessory protein soc around the threefold sites on the outer surface of the expanded surface lattice results in a substantial further stabilization (.DELTA.tm = +5.degree.). The interfaces between capsomers appear to be relatively weak points that are reinforced by clamp-like binding of soc. These results imply that the triplex proteins of other viruses (their structural counterparts of **soc**) are likely also to be involved in **capsid** stabilization. Cryo-electron microscopy was used to make conclusive interpretations of endotherms in terms of denaturation events. These data also revealed that the cleaved/unexpanded capsid has an angular polyhedral morphol. and has a pronounced relief on its outer surface. Moreover, it is 14% smaller in linear dimensions than the cleaved/expanded capsid, and its shell is commensurately thicker.

IT Thermodynamics
(of bacteriophage T4 **capsid** expansion, stabilization by protein **soc** binding and conformational changes of **capsid** protein gp23 in relation to)

IT Conformation and Conformers
(of capsid protein gp23, in bacteriophage T4 capsid expansion)

IT Virus, bacterial
(T4, **capsid** expansion of, thermodn. studies of, **capsid** protein gp23 conformational changes and stabilization by proteins **soc** in relation to)

IT Virion structure
(**capsid**, expansion of, of bacteriophage T4, **capsid** protein gp23 conformational changes in and protein **soc** binding stabilization of)

IT Proteins, specific or class

RL: BIOL (Biological study)
(capsid, gp23, conformational changes of, in bacteriophage T4 capsid expansion, thermodn. in relation to)
IT Proteins, specific or class
RL: BIOL (Biological study)
(gene **soc**, binding of, to **capsid** of bacteriophage T4, stabilization of **capsid** expansion in relation to)

L12 ANSWER 6 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1993:17149 CAPLUS
DOCUMENT NUMBER: 118:17149
TITLE: Construction of a chimeric viral gene expressing plum pox virus coat protein
AUTHOR(S): Ravelonandro, Michel; Monsion, Marie; Teycheney, Pierre Yves; Delbos, Rene; Dunez, Jean
CORPORATE SOURCE: Stn. Pathol. Veg., INRA, Villenave d'Ornon, 33883, Fr.
SOURCE: Gene (1992), 120(2), 167-73
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The **capsid**-encoding gene of plum pox virus (PPV) was fused with the leader sequence of the coat protein mRNA (cp) of tobacco mosaic virus by a novel mutagenesis technique which involves reverse transcription of minus-strand RNA [synthesized by in vitro transcription of a double-stranded (ds) cDNA clone], using an ad **hoc** synthetic oligodeoxynucleotide as primer. The **capsid**-encoding gene of plum pox virus (PPV) was fused with the leader sequence of the coat protein mRNA (cp) of tobacco mosaic virus by a novel mutagenesis technique which involves reverse transcription of minus-strand RNA (synthesized by in vitro transcription of a double-stranded (ds) cDNA clone), using an ad **hoc** synthetic oligodeoxynucleotide as primer. The resulting cDNA was rendered ds and cloned into the plasmid, pBluescribe M13+. Transcription of this chimeric construction produced RNA mols. of 1250 nucleotides in length, which were used as messengers in the in vitro protein-synthesizing systems. The major product of this transcript consists of a 36-kDa polypeptide and was identified as the PPV coat protein (CP) by mol. wt. estn. and by immunopptn. with a polyclonal antiserum to PPV. Transfer of this cDNA vis Agrobacterium tumefaciens into plants was successfully performed. Transgenic Nicotiana plants producing the PPV CP were subsequently obtained.
IT Mutation
(method for, using RNA transcript as template)
IT Tobacco
(transgenic, plum pox virus coat protein expression in)
IT Proteins, specific or class

RL: BIOL (Biological study)
(TMVP (tobacco mosaic virus coat protein), fusion products, with plum pox virus coat protein, construction and expression of)

IT Gene, microbial
RL: BIOL (Biological study)
(chimeric, for coat protein of plum pox virus and coat protein leader sequence of tobacco mosaic virus, construction and expression of)

IT Proteins, specific or class
RL: BIOL (Biological study)
(coat, fusion products, of plum pox virus with coat protein leader sequence from tobacco mosaic virus, construction and expression of)

IT Virus, plant
(plum pox, coat protein of, construction of chimeric gene expressing)

IT Virus, plant
(tobacco mosaic, coat protein leader sequence of, fusion to plum pox virus coat protein of)

IT Gene, microbial
RL: BIOL (Biological study)
(cp, for coat protein, of plum pox virus, cloning and expression in transgenic tobacco of)

L12 ANSWER 7 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1990:527274 CAPLUS
DOCUMENT NUMBER: 113:127274
TITLE: The bacteriophage T4 gene mrh whose product inhibits late T4 gene expression in an Escherichia coli rpoH (.sigma.32) mutant
AUTHOR(S): Frazier, Mark W.; Mosig, Gisela
CORPORATE SOURCE: Dep. Mol. Biol., Vanderbilt Univ., Nashville, TN, 37235, USA
SOURCE: Gene (1990), 88(1), 7-14
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In an E. coli rpoH mutant (affecting .sigma.32, heat-shock sigma factor) infected at high temps. with wild-type T4 phage, late T4 transcription and consequently progeny prodn. are dramatically impaired. This defect is due, in part, to insufficient activity of .sigma.70, which is necessary to initiate early T4 transcription. Unexpectedly, however, in this rpoH host, late T4 transcription is also impaired when the temp. is raised from 30 to 42.degree. late after infection, when T4 transcription is directed by the T4-encoded sigma factor, .sigma.gp55. A T4 gene designated mrh (modulates rpoH), located at 14 kb on the T4 map, is responsible for the inhibition of late T4 transcription in the rpoH mutant host. T4 deletion mutants that lack the mrh gene can produce progeny in the

rpoH host, but the Mrh protein, provided in trans from a plasmid-borne mrh gene, inhibits this growth. This T4 gene was cloned and sequenced and the Mrh protein prepd. in a T7 RNA polymerase-dependent expression system. The Mr of the Mrh protein deduced from the nucleotide sequence is 13,419. Gene mrh is cotranscribed with several other, yet unidentified genes, both from an early promoter downstream from the late **soc** gene (encoding the **small outer capsid** protein) and from the late **soc** promoter further upstream. The mrh transcript initiated at the late promoter requires antitermination downstream from soc at a palindromic sequence that could fold into a stable hairpin contg. a CUUCGG loop and that terminates most, if not all, transcripts initiated from early promoters further upstream.

IT Escherichia coli
(gene rpoH mutant of, phage T4 late gene expression in, gene mrh inhibition of)

IT Protein sequences
(of gene mrh protein, of phage T4, complete)

IT Protein sequences
(of gene soc.-1 protein, of phage T4, complete)

IT Microorganism development
(of phage T4, gene mrh in regulation of)

IT Proteins, specific or class
RL: PROC (Process)
(Mrh (modulator of RNA formation factor .sigma.-32), of phage T4, sequence and regulatory function of)

IT Virus, bacterial
(T4, genes mrh and soc-1 of, sequence and function of)

IT Proteins, specific or class
RL: BIOL (Biological study)
(gene soc.-1, of phage T4, amino acid sequence of)

IT Deoxyribonucleic acid sequences
(gene soc.-1 protein-specifying, of phage T4, complete)

IT Gene and Genetic element, microbial
RL: PROC (Process)
(late, of phage T4, gene mrh protein in regulation of)

IT Deoxyribonucleic acid sequences
(protein Mhr-specifying, of phage T4, complete)

IT Gene and Genetic element, microbial
RL: PROC (Process)
(mrh, of phage T4, sequence and function of)

IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(rpoH, for RNA formation factor .sigma.32, of Escherichia coli, mutation in, phage T4 gene mrh protein effect on)

IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(**soc**, for **small outer**

capsid protein, of phage T4, early and late promoter regions of, gene mrh transcription in relation to)

IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(soc.-1, of phage T4, nucleotide and encoded peptide sequences of)

IT 129288-93-3, Protein (bacteriophage T4 clone pMFs37 gene soc.-1)
129289-54-9, Protein (bacteriophage T4 clone pMF28 gene mrh)
RL: PRP (Properties)
(amino acid sequence of)

IT 129289-03-8, Deoxyribonucleic acid (bacteriophage T4 clone pMF28 gene mrh) 129289-04-9, Deoxyribonucleic acid (bacteriophage T4 clone pMF26 protein gene) 129289-05-0, Deoxyribonucleic acid (bacteriophage T4 clone pMFs37 gene soc.-1) 129289-06-1, Deoxyribonucleic acid (bacteriophage T4 clone pMFs37 protein gene)
RL: BIOL (Biological study); PRP (Properties)
(nucleotide sequence of)

L12 ANSWER 8 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1985:450955 CAPLUS
DOCUMENT NUMBER: 103:50955
TITLE: Assembly-dependent conformational changes in a viral capsid protein. Calorimetric comparison of successive conformational states of the gp23 surface lattice of bacteriophage T4
AUTHOR(S): Ross, Philip D.; Black, Lindsay W.; Bisher, Margaret E.; Steven, Alasdair C.
CORPORATE SOURCE: Lab. Mol. Biol., Natl. Inst. Arthritis, Diabetes Dig. Kidney Dis., Bethesda, MD, 20205, USA
SOURCE: J. Mol. Biol. (1985), 183(3), 353-64
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Inter- and intrasubunit bonding within the surface lattice of the capsid of bacteriophage T4 was investigated by differential scanning calorimetry of polyheads, in conjunction with electron microscopy, limited proteolysis, and SDS-polyacrylamide gel electrophoresis. The bonding changes corresponding to successive stages of assembly of the major capsid protein gp23, including its maturation cleavage, were similarly characterized. The uncleaved/unexpanded surface lattice exhibited 2 endothermic transitions. The minor event, at 46.degree., did not visibly affect the surface lattice morphol. and probably represents denaturation of the N-terminal domain of gp23. The major endotherm, at 65.degree., represents denaturation of the gp23 polymers. Sol. gp23 from dissocd. polyheads was extremely unstable and exhibited no endotherm. Cleavage of gp23 to gp23* and the ensuing expansion transformation effected a major stabilization of the surface lattice of polyheads, with single endotherms whose m.p. (tm*) ranged 73-81.degree. depending upon the mutant used and

the fraction of gp23 that was cleaved to gp23* prior to expansion. Binding of the accessory proteins soc and hoc further modulated the thermograms of cleaved/expanded polyheads, and their effects were additive. Binding of hoc conferred a new minor endotherm at 68.degree. corresponding to at least partial denaturation of hoc. Denatured hoc nevertheless remained assocd., with the surface lattice although in an altered, protease-sensitive state which correlated with delocalization of hoc subunits visualized in filtered images. While hoc binding had little effect on thermal stability of the gp23* matrix, soc binding further stabilized the surface lattice (.DELTA.Hd .apprx.+50%; .DELTA.tm* = +5.5.degree.). In all states of the surface lattice, the inter- and intrasubunit bonding configurations of gp23 appeared to be coordinated to be of similar thermal stability. Thermodynamically, the expansion transformation was characterized by .DELTA.H .mchlt. 0; .DELTA.Cp .apprx. 0, suggesting enhancement of van der Waals' and(or) H-bonding interactions, together with an increased exposure to solvent of hydrophobic residues of gp23* in the expanded state. These findings illuminate hypotheses of capsid assembly based on conformational properties of gp23: inter alia, they indicate a role for the N-terminal portion of gp23 in regulating polymn., and force a reappraisal of models of capsid swelling based on the swivelling of conserved domains.

IT Thermodynamics
(of conformational transitions, in phage T4 capsid)

IT Conformation and Conformers
(of protein gp23 surface lattice, thermal transitions of)

IT Virus, bacterial
(T4, capsid protein of, thermal stability of)

IT Proteins
RL: BIOL (Biological study)
(gene 23, capsid, of phage T4, thermal stability of)

IT Proteins
RL: BIOL (Biological study)
(gene **hoc**, in phage T7 **capsids**, assembly-dependent conformational changes in relation to)

IT Proteins
RL: BIOL (Biological study)
(gene **soc**, in phage T7 **capsids**, assembly-dependent conformational changes in relation to)

L12 ANSWER 9 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1985:107213 CAPLUS
DOCUMENT NUMBER: 102:107213
TITLE: Regulation of a new bacteriophage T4 gene, 69, that spans an origin of DNA replication
AUTHOR(S): Macdonald, Paul M.; Mosig, Gisela
CORPORATE SOURCE: Dep. Mol. Biol., Vanderbilt Univ., Nashville, TN, 37235, USA

Searcher : Shears 308-4994

SOURCE: EMBO J. (1984), 3(12), 2863-71
CODEN: EMJODG; ISSN: 0261-4189
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The DNA sequence and transcription patterns in a 3-kilobase (kb) segment between 15 and 18 kb on the std. phage T4 map and spanning an origin of DNA replication were detd. A new gene, 69, spans this origin. Gene 69 codes for 2 overlapping proteins that share a common C-terminal segment. Defective DNA replication in an appropriate amber mutant shows that at least the larger of the 2 proteins is required for efficient T4 DNA replication. The 2 proteins encoded by gene 69 are expressed from different transcripts that are under different regulation. The smaller protein, gp69*, can be expressed immediately from an Escherichia coli-like promoter, whereas expression of the larger protein, gp69, must be delayed, since its middle promoter requires T4-encoded proteins, most likely gpmot, for activation. The possible significance of 2 overlapping proteins in the assembly of replisomes is discussed. Gene 69 is bracketed by the nonessential early gene dam (DNA adenine methylase) and the late gene **soc** (**small outer capsid** protein). Transcripts through this region are interdigitated in a complex pattern, which reveals all elements that are thought to be important in regulation of prereplicative and postreplicative T4 genes.

IT Protein sequences
(of DNA adenine methylase, of phage T4, complete)
IT Protein sequences
(of gene 69 protein, of phage T4, complete)
IT Protein sequences
(of gene 69* protein, of phage T4, complete)
IT Protein sequences
(of gene soc protein, of phage T4, complete)
IT Deoxyribonucleic acid sequences
(DNA adenine methyltransferase-specifying, of phage T4, complete)
IT Virus, bacterial
(T4, gene 69 and 69* of, nucleotide and encoded amino acid sequences and gene mot regulation of)
IT Deoxyribonucleic acid sequences
(gene 69 protein-specifying, of phage T4, complete)
IT Deoxyribonucleic acid sequences
(gene 69* protein-specifying, of phage T4, complete)
IT Deoxyribonucleic acid sequences
(gene soc protein-specifying, of phage T4, complete)
IT Gene and Genetic element, microbial
RL: PROC (Process)
(69; of phage T4, sequence and gene mot regulation of)
IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(mot, of phage T4, genes 69 and 69* regulation by)

IT 66813-42-1 95229-15-5 95229-88-2 95229-89-3
RL: PRP (Properties)
(amino acid sequence of)
IT 88997-34-6 95229-29-1 95229-30-4 95229-31-5
RL: BIOL (Biological study); PRP (Properties)
(nucleotide sequence of)
IT 69553-52-2
RL: PRP (Properties)
(of phage T4, sequence of)

L12 ANSWER 10 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1980:617773 CAPLUS
DOCUMENT NUMBER: 93:217773
TITLE: Effect of hoc protein on the electrophoretic mobility of intact bacteriophage T4D particles in polyacrylamide gel electrophoresis
AUTHOR(S): Childs, J. D.
CORPORATE SOURCE: Radiat. Biol. Branch, At. Energy Canada Ltd., Chalk River, ON, K0J 1J0, Can.
SOURCE: J. Mol. Biol. (1980), 141(2), 163-73
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The electrophoretic mobility of intact bacteriophage T4D particles lacking a nonessential head protein, hoc, was 24% faster than wild-type particles in 1.85% polyacrylamide gels at pH 8.3. Another nonessential outer **capsid** protein, **soc**, did not appear to influence the electrophoretic mobility of phage particles either in the presence or absence of **hoc** protein. A previously isolated electrophoretic mutant, eph1, which migrated 14% more slowly than wild type, had immunol. detectable hoc protein, and appeared to affect electrophoretic mobility by changing the net charge of phage particles. Both eph1 and hoc are located between genes 24 and 25 adjacent to a continuous sequence of head assembly genes (20 to 24). Particles from a mixed infection of eph1 and eph+ migrated as a diffuse band with mobility intermediate between eph1 and eph+. Thus, phenotypic mixing probably occurred, producing hybrid phage particles contg. random amts. of mutant and normal eph protein. Complementation tests based on phenotypic mixing ruled out the possibility that the eph1 mutation is in genes 24 or 25 and showed that it is probably a missense hoc mutant.
IT Virus, bacterial
(T4D, electrophoretic mobility of, hoc protein effect on)
IT Proteins
(hoc, of bacteriophage T4D, electrophoretic mobility in relation to)
IT Gene
(eph1, for bacteriophage T4D head proteins)
IT Gene

(hoc, for bacteriophage T4D head proteins)

L12 ANSWER 11 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1980:617639 CAPLUS
DOCUMENT NUMBER: 93:217639
TITLE: Head shell protein hoc alters the surface charge of bacteriophage T4. Composite slab gel electrophoresis of phage T4 and related particles
AUTHOR(S): Yamaguchi, Yasuhiro; Yanagida, Mitsuhiro
CORPORATE SOURCE: Dep. Biophys., Kyoto Univ., Kyoto, 606, Japan
SOURCE: J. Mol. Biol. (1980), 141(2), 175-93
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In electrophoresis, bacteriophages T4 **hoc** (a T4 mutant), wild-type T2, T6, and RB69, all of which lack the nonessential head shell protein, **hoc** (**highly** antigenic **outer capsid** protein), migrated more rapidly at pH 8.3 than T4 **hoc+** and other RB strains. This effect appeared to be primarily due to a net charge difference, not to differences in wt. or shape. T4 hoc phages partially reconstituted with isolated hoc protein gave a single electrophoretic band with a mobility between hoc and hoc+ phages, supporting a noncooperative binding model. The binding velocity was proportional to hoc concn. and the ratio of unbound to total no. of binding sites. T4 hoc phages aggregated reversibly at low ionic strength to form large clumps; Mg or Ca inhibited aggregation. Thus, hoc protein may be involved in keeping the interaction between phages to a min. Electrophoretic properties of structural parts of phage T4, various phages, and protein assemblies are described. The composite gel system may be useful for studies on viruses and supramols.
IT Virus, bacterial
(T4, hoc protein of, surface chem. in relation to)
IT Proteins
(hoc, of bacteriophage T4, surface chem. in relation to)

L12 ANSWER 12 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1978:543230 CAPLUS
DOCUMENT NUMBER: 89:143230
TITLE: Isolation and characterization of bacteriophage T4 mutant preheads
AUTHOR(S): Onorato, Louise; Stirmer, Branka; Showe, Michael K.
CORPORATE SOURCE: Dep. Microbiol., Univ. Basel, Basel, Switz.
SOURCE: J. Virol. (1978), 27(2), 409-26
CODEN: JOVIAM; ISSN: 0022-538X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To det. the function of individual gene products in the assembly and maturation of T4 prehead, aberrant preheads produced by mutations in 3 of the T4 head genes were isolated and characterized. Mutants in gene 21, which codes for T4 maturation protease, produced rather stable preheads whose morphol. and protein compn. were consistent with a wild-type prehead blocked in maturation cleavages. Mutants in gene 24 produced similar structures which were unstable because they have gaps at all of their icosahedral vertexes except the membrane attachment site. In addn., greatly elongated giant preheads were produced, suggesting that in the absence of P24 at the vertexes, the distal cap of the prehead was unstable, allowing abnormal elongation of both the prehead core and its shell. Vertex completion by P24 was required to allow maturation cleavages to occur, and 24- preheads could be matured to capsids in vitro by addn. of P24. Preheads produced by a temp. sensitive mutant in gene 23 were deficient in core proteins. The shell of these preheads had the expanded lattice characteristic of the mature **capsid** as well as the binding sites for proteins **hoc** and **soc**, even though none of the maturation cleavage took place. The 21- preheads composed of wild-type P23 could be expanded in vitro without cleavage.

IT Gene
RL: BIOL (Biological study)
(in phage T4 capsid precursor maturation)

IT Virus, bacterial
(T4, capsid precursor maturation by, genes in)

L12 ANSWER 13 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1978:438292 CAPLUS
DOCUMENT NUMBER: 89:38292
TITLE: Complete primary structure of the **small outer capsid** (**soc**) protein of bacteriophage T4
AUTHOR(S): Bijlenga, Rudolf K. L.; Ishii, Tetsuro; Tsugita, Akira
CORPORATE SOURCE: Biozent., Univ. Basel, Basel, Switz.
SOURCE: J. Mol. Biol. (1978), 120(2), 249-63
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The complete amino acid sequence of the soc protein of bacteriophage T4 was detd. by std. sequencing techniques. The protein has 85 residues and a mol. wt. of 9700. The S-contg. amino acids are absent and the soc protein can be classed as hydrophobic, although the no. of nonpolar residues is not particularly high. Prediction of the secondary structure suggests that soc protein may have 40-50 residues in 5 .alpha.-helical regions, 23 residues may be distributed among 4 .beta.-pleated sheets, and 2 .beta.-turns can be expected.

IT Peptides, properties
RL: PRP (Properties)
(amino acid sequence of, of protein (phage T4 outer capsid))
IT Chains, chemical
(conformation of, of phage T4 outer capsid protein)
IT Molecular structure, natural product
(of protein (phage T4 outer capsid))
IT Virus, bacterial
(T4, outer capsid protein of, amino acid sequence of)
IT 66813-42-1
RL: PRP (Properties)
(amino acid sequence of)

L12 ANSWER 14 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1978:420190 CAPLUS
DOCUMENT NUMBER: 89:20190
TITLE: Binding of the structural protein soc to the head shell of bacteriophage T4
AUTHOR(S): Ishii, Tetsuro; Yamaguchi, Yasuhiro; Yanagida, Mitsuhiro
CORPORATE SOURCE: Fac. Sci., Kyoto Univ., Kyoto, Japan
SOURCE: J. Mol. Biol. (1978), 120(4), 533-44
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Kinetic expts. on the binding of the **small outer capsid** protein **soc** to the head shell of phage T4 were conducted. The relation between the binding velocity V, the soc concn., and the ratio f of unoccupied to total binding sites is approx. V .varies. [soc]1.4 .times. f2.2 at 37.degree.: the rate of binding decreases sharply as the reaction proceeds. The reaction is rather complex, interpreted either as the binding to the sites of different affinity for soc or as neg. concerted binding. In contrast, the **highly** antigenic **outer capsid** protein **hoc** seems to bind to identical and independent binding sites, because the relation V .varies. [**hoc**] .times. f was obtained. Expts. using the double mutant T4soc hoc indicated that soc and hoc binding are mutually independent, at least under these exptl. conditions.
IT Virus, bacterial
(T4, head proteins of, binding kinetics of)
IT Proteins
(hoc, binding kinetics of, to phage T4 heads)
IT Proteins
(soc, binding kinetics of, to phage T4 heads)

L12 ANSWER 15 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1978:420044 CAPLUS
DOCUMENT NUMBER: 89:20044

TITLE: Head maturation pathway of bacteriophages T4 and T2. IV. In vitro transformation of T4 head-related particles produced by mutants in gene 17 to capsid-like structures
AUTHOR(S): Carrascosa, Jose L.
CORPORATE SOURCE: Biozent., Univ. Basel, Basel, Switz.
SOURCE: J. Virol. (1978), 26(2), 420-8
CODEN: JOVIAM; ISSN: 0022-538X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB T4 mutants in gene 17 accumulate particles which contain the main head protein in the cleaved form (gp23*) arranged in an unexpanded lattice (empty small particles), together with other expanded capsids (empty large particles). The isolated empty small particles can be transformed in vitro, by lowering the ionic strength, to capsid-like structures. This structural transformation is not coupled to chem. modification of the structural proteins of the empty small particles. In contrast to unexpanded particles that are easily dissocd., the transformed structures are as resistant to dissocn. as other T-even head-related particles with expanded lattice. Furthermore, the transformed particles are able to bind in vitro **hoc** and **soc** proteins, rendering **capsids** indistinguishable from the normal T4 **capsids** both morphol. and by their stability against denaturing agents. The results indicate that the in vitro transformation of the empty small particles might mimic important and characteristic aspects of the in vivo maturation of T4 heads, thus suggesting a possible role of the cleaved but unexpanded particle in the maturation pathway of the T4 shell.

IT Glycoproteins
RL: BIOL (Biological study)
(viral, T4 capsid maturation with cleaved)

IT Virus, bacterial
(T4, capsid maturation of, with cleaved glycoprotein)

L12 ANSWER 16 OF 17 CAPLUS COPYRIGHT 1999 ACS
ACCESSION NUMBER: 1977:435517 CAPLUS
DOCUMENT NUMBER: 87:35517
TITLE: Comparison of the structural and chemical composition of giant T-even phage heads
AUTHOR(S): Aebi, U.; Bijlenga, R. K. L.; Ten Heggeler, B.; Kistler, J.; Steven, A. C.; Smith, P. R.
CORPORATE SOURCE: Biozent., Univ. Basel, Basel, Switz.
SOURCE: J. Supramol. Struct. (1976), 5(4), 475-95
CODEN: JSPMAW
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A study has been made of the structure of the capsids of T4D giant phage produced from mutants in gene 23 and temp.-sensitive mutants

in gene 24, and T4D and T2L giant phage formed by the addn. of L-canavanine followed by an L-arginine chase in the growth medium. All the giant phage capsids are built according to the same geometrical architecture. This consists of a near-hexagonal surface net, lattice const. 129.5 .ANG., folded into a left-handed T = 13 prolate icosahedron elongated along 1 of its 5-fold symmetry axes. Their only apparent difference from wild-type T-even phage capsids is their abnormally elongated tubular part. A comparison of the capsomere morphols. and protein compns. of the giant phage capsids showed that all T4D giants are identical but differ from T2L. The T4D capsomere has a complex (6 + 6 + 1)-type morphol., whereas the T2L has a simple 6-type. T2L phage, however, lack 2 **capsid** proteins, **soc** and **hoc**, present in T4D. The difference in capsomere morphol. can therefore be related to the difference in the protein compns. of these 2 phage.

IT Proteins
RL: BIOL (Biological study)
(viral capsid, of giant phages T4D and T2L)

IT Virus, bacterial
(T2L, capsids of giant, structure and compn. of)

IT Virus, bacterial
(T4D, capsids of giant, structure and compn. of)

L12 ANSWER 17 OF 17 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER:	1977:185585 CAPLUS
DOCUMENT NUMBER:	86:185585
TITLE:	Capsid fine structure of T-even bacteriophages. Binding and localization of two dispensable capsid proteins into the P23* surface lattice
AUTHOR(S):	Aebi, U.; Van Driel, R.; Bijlenga, R. K. L.; Ten Heggeler, B.; Van den Broek, R.; Steven, A. C.; Smith, P. R.
CORPORATE SOURCE:	Biozent., Univ. Basel, Basel, Switz.
SOURCE:	J. Mol. Biol. (1977), 110(4), 687-98 CODEN: JMOBAK
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB Two methods were used to identify the stain-excluding regions in the P23* matrix of the T-even phage **capsid**, and to investigate the bonding of the dispensable proteins **hoc** and **soc** into this matrix. T2L giant phage **capsids**, which lack **hoc** and **soc**, were titrated with these 2 proteins. The **hoc**, **soc** and other **capsid** proteins were differentially dissocd. from T4D and from **hoc** and **soc**-complemented T2L **capsids** by reversible acylation with citraconic anhydride. Changes in the capsomeres of giant capsids were monitored by electron microscopy followed by optical filtration of the electron monographs. Apparently the stain-excluding region in the center of

the capsomere is assocd. with binding of 1 mol. of hoc protein, and the 6 stain-excluding regions bridging adjacent capsomeres are assocd. with the binding of 6 mols. of soc protein. The binding of soc in the absence of hoc was highly cooperative, whereas the presence of hoc in the P23* lattice induced a marked heterogeneity in the soc binding sites.

IT Proteins
RL: BIOL (Biological study)
(of bacteriophage surface lattice P23*)

IT Virus, bacterial
(T-even, dispensable capsid proteins of P23* lattice of)

=> d his l13-; d 1-39 ibib abs

(FILE 'MEDLINE, BIOSIS, EMBASE, LIFESCI, BIOTECHDS, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, PROMT' ENTERED AT 16:12:07 ON 02 AUG 1999)

L13 109 S L11
L14 81 S L13 NOT L7
L15 39 DUP REM L14 (42 DUPLICATES REMOVED)

L15 ANSWER 1 OF 39 SCISEARCH COPYRIGHT 1999 ISI (R)
ACCESSION NUMBER: 1999:478370 SCISEARCH
THE GENUINE ARTICLE: 207BB
TITLE: Analysis of capsid portal protein and terminase functional domains: Interaction sites required for DNA packaging in bacteriophage T4
AUTHOR: Lin H C; Rao V B; Black L W (Reprint)
CORPORATE SOURCE: UNIV MARYLAND, DEPT BIOCHEM & MOL BIOL, BALTIMORE, MD 21201 (Reprint); UNIV MARYLAND, DEPT BIOCHEM & MOL BIOL, BALTIMORE, MD 21201
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (4 JUN 1999) Vol. 289, No. 2, pp. 249-260.
Publisher: ACADEMIC PRESS LTD, 24-28 OVAL RD, LONDON NW1 7DX, ENGLAND.
ISSN: 0022-2836.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 40

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Bacteriophage DNA packaging results from an ATP-driven translocation of concatemeric DNA into the prohead by the phage terminase complexed with the portal vertex dodecamer of the prohead. Functional domains of the bacteriophage T4 terminase and portal gene 20 product (gp20) were determined by mutant analysis and sequence localization within the structural genes. Interaction regions of the portal vertex and large terminase subunit (gp17) were determined by genetic (terminase-portal intergenic suppressor mutations),

biochemical (column retention of gp17 and inhibition of in vitro DNA packaging by gp20 peptides), and immunological (co-immunoprecipitation of polymerized gp20 peptide and gp17) studies. The specificity of the interaction was tested by means of a phage T4 **HOC** (**highly** antigenic **outer** **capsid** protein) display system in which wild-type, cs20, and scrambled portal peptide sequences were displayed on the **HOC** protein of phage T4. Binding affinities of these recombinant phages as determined by the retention of these phages by a His-tag immobilized gp17 column, and by co-immunoprecipitation with purified terminase supported the specific nature of the portal protein and terminase inter action sites. Ln further support of specificity, a gp20 peptide corresponding to a portion of the identified site inhibited packaging whereas the scrambled sequence peptide did not block DNA packaging in vitro. The portal interaction site is localized to 28 residues in the central portion of the linear sequence of gp20 (524 residues). As judged by two pairs of intergenic portal-terminase suppressor mutations, two separate regions of the terminase large subunit gp17 (central and COOH-terminal) interact through hydrophobic contacts at the portal site. Although the terminase apparently interacts with this gp20 portal peptide, polyclonal antibody against the portal peptide appears unable to access it in the native structure, suggesting intimate association of gp20 and gp17 possibly internalizes terminase regions within the portal in the packasome complex. Both similarities and differences are seen in comparison to analogous sites which have been identified in phages T3 and lambda. (C) 1999 Academic Press.

L15 ANSWER 2 OF 39 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 1998086228 MEDLINE
DOCUMENT NUMBER: 98086228
TITLE: Evidence of viral capsid dynamics using limited proteolysis and mass spectrometry.
AUTHOR: Bothner B; Dong X F; Bibbs L; Johnson J E; Siuzdak G
CORPORATE SOURCE: Department of Molecular Biology, The Scripps Research Institute, La Jolla, California 92037, USA.
CONTRACT NUMBER: 1 S10 RR07273-01 (NCRR)
5 P01 GM48870-05 (NIGMS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Jan 9) 273 (2) 673-6.
Journal code: HIV. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
ENTRY MONTH: 199804
ENTRY WEEK: 19980402
AB Virus particles are stable yet exhibit highly dynamic character

given the events that shape their life cycle. Isolated from their hosts, the nucleoprotein particles are macromolecules that can be crystallized and studied by x-ray diffraction. During assembly, maturation and entry, however, they are highly dynamic and display remarkable plasticity. These dynamic properties can only be inferred from the x-ray structure and must be studied by methods that are sensitive to mobility. We have used matrix-assisted laser desorption/ionization mass spectrometry combined with time resolved, limited proteolysis (Cohen, S. L., Ferre-D'Amare, A. R., Burley, S. K., and Chait, B. T. (1995) Protein Sci. 4, 1088-1099; Kriwacki, R. W., Wu, J., Tennant, T., Wright, P. E., and Siuzdak, G. (1997) J. Chromatogr. 777, 23-30; Kriwacki, R. W., Wu, J., Siuzdak, G., and Wright, P. E. (1996) J. Am. Chem. **Soc**. 118, 5320-5321) to examine the viral **capsid** of flock house virus. Employing less than 10 microg of virus, time course digestion products were assigned to polypeptides of the subunit. Although surface regions in the three-dimensional structure were susceptible to cleavage on extended exposure to the protease, the first digestion products were invariably from parts of the subunit that are internal to the x-ray structure. Regions in the N- and C-terminal portions of the subunit, located within the shell in the x-ray structure, but implicated in RNA neutralization and RNA release and delivery, respectively, were the most susceptible to cleavage demonstrating transient exposure of these polypeptides to the viral surface.

L15 ANSWER 3 OF 39 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 97449307 MEDLINE
DOCUMENT NUMBER: 97449307
TITLE: Cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.
AUTHOR: Ren Z J; Baumann R G; Black L W
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Maryland School of Medicine, Baltimore 21201-1503, USA.
CONTRACT NUMBER: AI-11676 (NIAID)
SOURCE: GENE, (1997 Aug 22) 195 (2) 303-11.
Journal code: FOP. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199801
ENTRY WEEK: 19980104
AB A method was developed to clone linear DNAs by overexpressing T4 phage DNA ligase in vivo, based upon recombination deficient E. coli derivatives that carry a plasmid containing an inducible T4 DNA ligase gene. Integration of this ligase-plasmid into the chromosome of such E. coli allows standard plasmid isolation following linear

DNA transformation of the strains containing high levels of T4 DNA ligase. Intramolecular ligation allows high efficiency recircularization of cohesive and blunt-end terminated linear plasmid DNAs following transformation. Recombinant plasmids could be constructed in vivo by co-transformation with linearized vector plus insert DNAs, followed by intermolecular ligation in the T4 ligase strains to yield clones without deletions or rearrangements. Thus, in vitro packaged lox-site terminated plasmid DNAs injected from phage T4 were recircularized by T4 ligase in vivo with an efficiency comparable to CRE recombinase. Clones that expressed a **capsid**-binding 14-aa N-terminal peptide extension derivative of the **HOC** (**highly** antigenic **outer capsid**) protein for T4 phage **hoc** gene display were constructed by co-transformation with a linearized vector and a PCR-synthesized **hoc** gene. Therefore, the T4 DNA ligase strains are useful for cloning linear DNAs in vivo by transformation or transduction of DNAs with nonsequence-specific but compatible DNA ends.

L15 ANSWER 4 OF 39 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 97380582 MEDLINE
DOCUMENT NUMBER: 97380582
TITLE: A member of the immunoglobulin superfamily in bacteriophage T4.
AUTHOR: Bateman A; Eddy S R; Mesyanzhinov V V
CORPORATE SOURCE: MRC Laboratory of Molecular Biology, Cambridge, England.
SOURCE: VIRUS GENES, (1997) 14 (2) 163-5.
Journal code: XEI. ISSN: 0920-8569.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199711
ENTRY WEEK: 19971104
AB We report a prediction that the **highly** immunogenic **outer capsid** (**Hoc**) protein of the prokaryotic phage T4 contains three tandem immunoglobulin-like domains. Immunoglobulin-like folds have previously been identified in prokaryotic proteins but these share no recognizable sequence similarity with eukaryotic immunoglobulin superfamily (IgSF) folds, and may represent products of convergent evolution. In contrast, the **Hoc** immunoglobulin-like folds are proposed, based on immunoglobulin-like sequence consensus matches detected by hidden Markov modeling. We propose that the **Hoc** immunoglobulin-like domains and eukaryotic immunoglobulin-like domains are likely to be related by divergence from a common ancestor.

L15 ANSWER 5 OF 39 BIOSIS COPYRIGHT 1999 BIOSIS DUPLICATE 4
ACCESSION NUMBER: 1998:188889 BIOSIS
DOCUMENT NUMBER: PREV199800188889
TITLE: Studies on in vitro growth characteristics of human rotavirus serotype-3: A new substrate of buffalo green monkey kidney cells.
AUTHOR(S): Parida, M. M. (1); Pandya, G.; Bhargava, R.; Jana, A. M.
CORPORATE SOURCE: (1) Div. Virol. and Biotechnol., Defence Res. and Dev. Establishment, Jhansi Road, Gwalior-474002 India
SOURCE: Biomedical Letters, (1997) Vol. 56, No. 221, pp. 19-26.
ISSN: 0961-088X.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Primary and continuous cell cultures, predominantly of monkey kidney origin, facilitate the propagation of human rotaviruses (HRV). Buffalo green monkey kidney (BGM) cells, a continuous cell culture, were used as a new substrate for the propagation of HRV serotype-3 (SA-11 virus), after initial adaptation in foetal rhesus monkey kidney (MA-104) cells. The infectivity potential of MA-104 adapted SA-11 virus towards BGM cells was assessed up to the tenth passage and compared with MA-104 cells. The BGM cells appeared to be relatively more efficient in supporting the growth of SA-11 virus than MA-104 as shown by the high virus yield. The in vitro growth curve in both types of cells indicated a similar growth pattern with maximal virus yield at 24 h post-infection. The immunogenic polypeptide profile of SA-11 virus in MA-104 as well as BGM cells revealed the presence of a **highly** immunogenic **outer capsid** glycoprotein (VP7) with a molecular weight of 37.3 kD.

L15 ANSWER 6 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 97:283449 PROMT
TITLE: Human Papillomavirus "Serological and T-Helper Cell Responses to Human Papillomavirus Type 16 L1 in Women with Cervical Dysplasia or Cervical Carcinoma and in Healthy Controls." Journal of General Virology, April 1997;78(Part 4):917-923.
AUTHOR(S): Shepherd, P.S.
SOURCE: Cancer Weekly Plus, (19 May 1997) pp. N/A.
LANGUAGE: English
WORD COUNT: 333
FULL TEXT IS AVAILABLE IN THE ALL FORMAT
AB Luxton, J.C.; Rose, R.C.; Coletart, T.; Wilson, P.; Shepherd, P.S. According to the authors' abstract of an article published in Journal of General Virology, "In a cross-sectional study we have investigated serological and T-helper (Th) cell responses to human

papillomavirus type 16 (HPV-16) L1 in women with HPV-16 related diseases and related them to cervical histology and HPV DNA status. Using a virus-like particle (VLP) based ELISA to detect antibodies to the HPV-16 L1 **capsid** protein, 45% (33/73) of women with cervical dysplasia, 40% (2/5) of women with cervical cancer, 36% (4/11) of healthy adult female controls and 6% (2/35) of healthy children were found to be seropositive. Amongst women with cervical dysplasia, the highest levels of seropositivity were found in those who were HPV-16 DNA positive (60%, 15/25) or positive for any of the 'high-risk' HPV types, 16/18/33 (58%, 18/31), when compared with those with HPV type 'X' (25%, 5/20) or with healthy children (6%, 2/35; P less than 0.05 for all comparisons). There was a trend for women with cervical dysplasia to show an increased level of seropositivity with increasing grade of lesion. There was no direct correlation found between seropositivity and Th cell responses in all groups studied. However, a combined analysis of each individual's Th and B cell responses suggests that a Th1 pattern of response is predominant amongst healthy adult controls (80% of responders) but reduced in women with cervical dysplasia (55% of responders). A trend towards a decrease in Th1 type responses was also noted with increasing grade of dysplastic lesion. These findings provide further evidence for the importance of the Th response in the control of genital HPV infections." The corresponding author for this study is: PS Shepherd, United Med & Dent Sch, Sch Med, Dept Immunol, London SE1 9RT, England. For subscription information for this journal contact the publisher: **Soc** General Microbiology, Harvest House, 62 London Road, Reading, Berks, England RG1 5AS.

L15 ANSWER 7 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 97:256106 PROMT
TITLE: HIV Vaccines "Humoral, Mucosal, and Cellular Immunity in Response to a Human Immunodeficiency Virus Type 1 Immunogen Expressed by a Venezuelan Equine Encephalitis Virus Vaccine Vector."
AUTHOR(S): Caley, I.J.; Betts, M.R.; Irlbeck, D.M.
SOURCE: AIDS Weekly Plus, (5 May 1997) pp. N/A.
ISSN: 1069-1456.
LANGUAGE: English
WORD COUNT: 329
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Caley, I.J.; Betts, M.R.; Irlbeck, D.M.; Davis, N.L.; Swanstrom, R.; Frelinger, J.A.; Johnston, R.E.
Journal of Virology, April 1997;71(4):3031-3038.
According to the authors' abstract of an article published in Journal of Virology, "A molecularly cloned attenuated strain of Venezuelan equine encephalitis virus (VEE) has been genetically

configured as a replication-competent vaccine vector for the expression of heterologous viral proteins (N.L. Davis, K.W. Brown, and R.E. Johnston, J Virol. 70:3781-3787, 1996). The matrix/ **capsid** (MA/CA) coding domain of human immunodeficiency virus type 1 (HIV-1) was cloned into the VEE vector to determine the ability of a VEE vector to stimulate an anti-HIV immune response in mice. The VEE-MA/CA vector replicated rapidly in the cytoplasm of baby hamster kidney (BHK) cells and expressed large quantities of antigenically identifiable MA/CA protein. When injected subcutaneously into BALB/e mice, the vector invaded and replicated in the draining lymphoid tissues, expressing HIV-1 MA/CA at a site of potent immune activity. Anti-MA/CA immunoglobulin G (IgG) and IgA antibodies were present in serum of all immunized mice, and titers increased after a second booster inoculation. IgA antibodies specific for MA/CA were detected in vaginal washes of mice that received two subcutaneous immunizations. Cytotoxic T-lymphocyte responses specific for MA/CA were detected following immunization with the MA/CA-expressing VEE vector. These findings demonstrate the ability of a VEE-based vaccine vector system to stimulate a comprehensive humoral and cellular immune response. The multifaceted nature of this response makes VEE an attractive vaccine for immunization against virus infections such as HIV-1, for which the correlates of protective immunity remain unclear, but may include multiple components of the immune system." The corresponding author for this study is: RE Johnston, Univ N Carolina, Sch Med, Dept Microbiol & Immunol, Chapel Hill, NC 27599 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 8 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 97:274822 PROMT
TITLE: HIV Vaccines "Humoral, Mucosal, and Cellular Immunity in Response to a Human Immunodeficiency Virus Type 1 Immunogen Expressed by a Venezuelan Equine Encephalitis Virus Vaccine Vector."
SOURCE: Vaccine Weekly, (5 May 1997) pp. N/A.
ISSN: 1074-2921.
LANGUAGE: English
WORD COUNT: 329
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Caley, I.J.; Betts, M.R.; Irlbeck, D.M.; Davis, N.L.; Swanstrom, R.; Frelinger, J.A.; Johnston, R.E. Journal of Virology, April 1997;71(4):3031-3038.
According to the authors' abstract of an article published in Journal of Virology, "A molecularly cloned attenuated strain of Venezuelan equine encephalitis virus (VEE) has been genetically

configured as a replication-competent vaccine vector for the expression of heterologous viral proteins (N.L. Davis, K.W. Brown, and R.E. Johnston, J Virol. 70:3781-3787, 1996). The matrix/ **capsid** (MA/CA) coding domain of human immunodeficiency virus type 1 (HIV-1) was cloned into the VEE vector to determine the ability of a VEE vector to stimulate an anti-HIV immune response in mice. The VEE-MA/CA vector replicated rapidly in the cytoplasm of baby hamster kidney (BHK) cells and expressed large quantities of antigenically identifiable MA/CA protein. When injected subcutaneously into BALB/e mice, the vector invaded and replicated in the draining lymphoid tissues, expressing HIV-1 MA/CA at a site of potent immune activity. Anti-MA/CA immunoglobulin G (IgG) and IgA antibodies were present in serum of all immunized mice, and titers increased after a second booster inoculation. IgA antibodies specific for MA/CA were detected in vaginal washes of mice that received two subcutaneous immunizations. Cytotoxic T-lymphocyte responses specific for MA/CA were detected following immunization with the MA/CA-expressing VEE vector. These findings demonstrate the ability of a VEE-based vaccine vector system to stimulate a comprehensive humoral and cellular immune response. The multifaceted nature of this response makes VEE an attractive vaccine for immunization against virus infections such as HIV-1, for which the correlates of protective immunity remain unclear, but may include multiple components of the immune system." The corresponding author for this study is: RE Johnston, Univ N Carolina, Sch Med, Dept Microbiol & Immunol, Chapel Hill, NC 27599 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 9 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 97:290743 PROMT
TITLE: Human Papillomavirus "Serological and T-Helper Cell Responses to Human Papillomavirus Type 16 L1 in Women with Cervical Dysplasia or Cervical Carcinoma and in Healthy Controls."
SOURCE: Disease Weekly Plus, (19 May 1997) pp. N/A.
LANGUAGE: English
WORD COUNT: 343
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Luxton, J.C.; Rose, R.C.; Coletart, T.; Wilson, P.; Shepherd, P.S. Journal of General Virology, April 1997;78(Part 4):917-923. According to the authors' abstract of an article published in Journal of General Virology, "In a cross-sectional study we have investigated serological and T-helper (Th) cell responses to human papillomavirus type 16 (HPV-16) L1 in women with HPV-16 related diseases and related them to cervical histology and HPV DNA status.

Using a virus-like particle (VLP) based ELISA to detect antibodies to the HPV-16 L1 **capsid** protein, 45% (33/73) of women with cervical dysplasia, 40% (2/5) of women with cervical cancer, 36% (4/11) of healthy adult female controls and 6% (2/35) of healthy children were found to be seropositive. Amongst women with cervical dysplasia, the highest levels of seropositivity were found in those who were HPV-16 DNA positive (60%, 15/25) or positive for any of the 'high-risk' HPV types, 16/18/33 (58%, 18/31), when compared with those with HPV type 'X' (25%, 5/20) or with healthy children (6%, 2/35; P less than 0.05 for all comparisons). There was a trend for women with cervical dysplasia to show an increased level of seropositivity with increasing grade of lesion. There was no direct correlation found between seropositivity and Th cell responses in all groups studied. However, a combined analysis of each individual's Th and B cell responses suggests that a Th1 pattern of response is predominant amongst healthy adult controls (80% of responders) but reduced in women with cervical dysplasia (55% of responders). A trend towards a decrease in Th1 type responses was also noted with increasing grade of dysplastic lesion. These findings provide further evidence for the importance of the Th response in the control of genital HPV infections." The corresponding author for this study is: PS Shepherd, United Med & Dent Sch, Sch Med, Dept Immunol, London SE1 9RT, England. For subscription information for this journal contact the publisher: **Soc** General Microbiology, Harvest House, 62 London Road, Reading, Berks, England RG1 5AS.

L15 ANSWER 10 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 97:57375 PROMT
TITLE: Kaposi's sarcoma (KSHV) "Kaposi's sarcoma-Associated Herpesvirus Gene Expression in Endothelial (Spindle) Tumor Cells."
SOURCE: Disease Weekly Plus, (27 Jan 1997) pp. N/A.
LANGUAGE: English
WORD COUNT: 319
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Staskus, K.A.; Zhong, W.D.; Gebhard, K.; Herndier, B.; Wang, H.; Renne, R.; Beneke, J.; Pudney, J.; Anderson, D.J.; Ganem, D.; Hasse, A.T.
Journal of Virology, January 1997;71(1):715-719.
According to the authors' abstract of an article published in Journal of Virology, "The recent discovery of DNA sequences of a new human herpesvirus in Kaposi's sarcoma (KS) has fueled speculation that this virus might cause KS. The mere presence, however, of a virus in a complex multicellular tumor like KS could just as well be construed as evidence of a passenger agent. We sought stronger evidence linking the KS-associated herpesvirus (KSHV) to tumor

formation by using in situ hybridization to investigate the specificity, constancy, and timing of KSHV gene expression in KS tumor cells. Here we document expression of a 700-nucleotide viral RNA in every KS tumor examined, from the earliest histologically recognizable stage to advanced tumors in which the vast majority of identifiable spindle tumor cells contain this transcript. Two other KSHV RNAs were also detected in a smaller fraction of the tumor cells in all but the earliest lesion. These viral RNAs were expressed to relatively low levels in this subset; because one of these RNAs encodes a major viral **capsid** protein, these cells may be producing KSHV. We did not find these KSHV genes expressed in a variety of other tumors and proliferative processes, but we did detect viral gene expression in prostatic tissue, supporting a possible mechanism for sexual transmission of KSHV. The close relationship between KS and KSHV gene expression is consistent with the hypothesis that KSHV is directly involved in the etiology and pathogenesis of KS." The corresponding author for this study is: AT Hasse, Univ Minnesota, Dept Microbiol, Umhc 196, 420 Delaware St Se, Minneapolis, MN 55455 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 11 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 97:47961 PROMT
TITLE: Kaposi's sarcoma (KSHV) "Kaposi's sarcoma-Associated Herpesvirus Gene Expression in Endothelial (Spindle) Tumor Cells."
SOURCE: Cancer Weekly Plus, (27 Jan 1997) pp. N/A.
LANGUAGE: English
WORD COUNT: 319

FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Staskus, K.A.; Zhong, W.D.; Gebhard, K.; Herndier, B.; Wang, H.; Renne, R.; Beneke, J.; Pudney, J.; Anderson, D.J.; Ganem, D.; Hasse, A.T. Journal of Virology, January 1997;71(1):715-719.
According to the authors' abstract of an article published in Journal of Virology, "The recent discovery of DNA sequences of a new human herpesvirus in Kaposi's sarcoma (KS) has fueled speculation that this virus might cause KS. The mere presence, however, of a virus in a complex multicellular tumor like KS could just as well be construed as evidence of a passenger agent. We sought stronger evidence linking the KS-associated herpesvirus (KSHV) to tumor formation by using in situ hybridization to investigate the specificity, constancy, and timing of KSHV gene expression in KS tumor cells. Here we document expression of a 700-nucleotide viral RNA in every KS tumor examined, from the earliest histologically recognizable stage to advanced tumors in which the vast majority of identifiable spindle tumor cells contain this transcript. Two other

KSHV RNAs were also detected in a smaller fraction of the tumor cells in all but the earliest lesion. These viral RNAs were expressed to relatively low levels in this subset; because one of these RNAs encodes a major viral **capsid** protein, these cells may be producing KSHV. We did not find these KSHV genes expressed in a variety of other tumors and proliferative processes, but we did detect viral gene expression in prostatic tissue, supporting a possible mechanism for sexual transmission of KSHV. The close relationship between KS and KSHV gene expression is consistent with the hypothesis that KSHV is directly involved in the etiology and pathogenesis of KS." The corresponding author for this study is: AT Hasse, Univ Minnesota, Dept Microbiol, Umhc 196, 420 Delaware St Se, Minneapolis, MN 55455 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 12 OF 39 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 97035251 MEDLINE
DOCUMENT NUMBER: 97035251
TITLE: Phage display of intact domains at high copy number: a system based on **SOC**, the **small outer capsid** protein of bacteriophage T4.
AUTHOR: Ren Z J; Lewis G K; Wingfield P T; Locke E G; Steven A C; Black L W
CORPORATE SOURCE: Department of Biological Chemistry, University of Maryland School of Medicine, Baltimore 21201, USA.
SOURCE: PROTEIN SCIENCE, (1996 Sep) 5 (9) 1833-43.
Journal code: BNW. ISSN: 0961-8368.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199704
ENTRY WEEK: 19970402

AB Peptides fused to the coat proteins of filamentous phages have found widespread applications in antigen display, the construction of antibody libraries, and biopanning. However, such systems are limited in terms of the size and number of the peptides that may be incorporated without compromising the fusion proteins' capacity to self-assemble. We describe here a system in which the molecules to be displayed are bound to pre-assembled polymers. The polymers are T4 **capsids** and polyheads (tubular **capsid** variants) and the display molecules are derivatives of the dispensable **capsid** protein **SOC**. In one implementation, **SOC** and its fusion derivatives are expressed at high levels in Escherichia coli, purified in high yield, and then bound in vitro to separately isolated polyheads. In

the other, a positive selection vector forces integration of the modified **soc** gene into a **soc**-deleted T4 genome, leading to in vivo binding of the display protein to progeny virions. The system is demonstrated as applied to C-terminal fusions to **SOC** of (1) a tetrapeptide; (2) the 43-residue V3 loop domain of gp120, the human immunodeficiency virus type-1 (HIV-1) envelope glycoprotein; and (3) poliovirus VP1 **capsid** protein (312 residues). **SOC**-V3 displaying phage were highly antigenic in mice and produced antibodies reactive with native gp120. That the fusion protein binds correctly to the surface lattice was attested in averaged electron micrographs of polyheads. The **SOC** display system is capable of presenting up to approximately 10(3) copies per **capsid** and > 10(4) copies per polyhead of V3-sized domains. Phage displaying **SOC**-VP1 were isolated from a 1:10(6) mixture by two cycles of a simple biopanning procedure, indicating that proteins of at least 35 kDa may be accommodated.

L15 ANSWER 13 OF 39 BIOSIS COPYRIGHT 1999 BIOSIS DUPLICATE 6
ACCESSION NUMBER: 1996:261629 BIOSIS
DOCUMENT NUMBER: PREV199698817758
TITLE: Display of peptides, domains and proteins on **SOC**, the **small outer capsid** protein of bacteriophage T4.
AUTHOR(S): Ren, Z. J. (1); Lewis, G. (1); Wingfield, P. T.; Locke, E. G.; Steven, A. C.; Black, L. W. (1)
CORPORATE SOURCE: (1) Univ. Md. Sch. Med., Baltimore, MD 21201 USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (1996) Vol. 96, No. 0, pp. 576.
Meeting Info.: 96th General Meeting of the American Society for Microbiology New Orleans, Louisiana, USA May 19-23, 1996
ISSN: 1060-2011.
DOCUMENT TYPE: Conference
LANGUAGE: English

L15 ANSWER 14 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 96:86895 PROMT
TITLE: Kaposi's Sarcoma Herpesvirus Moore, P.S.; Gao, S.J.; Dominguez, G.; Cesarman, E.; Lungu, O.; Knowles, D.M.; Garber, R.; Pellett, P.E.; Mcgeoch, D.J.; Chang, Y. "Primary Characterization of a Herpesvirus Agent Associated with Kaposi's sarcoma." Journal of Virology, January 1996;70(1):549-558.
SOURCE: Blood Weekly, (29 Jan 1996) pp. N/A.
ISSN: 1065-6073.
LANGUAGE: English

WORD COUNT: 296

FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB According to the authors' abstract of an article published in Journal of Virology, "Detection of novel DNA sequences in Kaposi's sarcoma (KS) and AIDS-related body cavity-based, non-Hodgkin's lymphomas suggests that these neoplasms are caused by a previously unidentified human herpesvirus. We have characterized this agent using a continuously infected B-lymphocyte cell line derived from an AIDS-related lymphoma and a genomic library made from a KS lesion, In this cell line, the agent has a large episomal genome with an electrophoretic mobility similar to that of 270-kb linear DNA markers during clamped homogeneous electric field gel electrophoresis. A 20.7-kb region of the genome has been completely sequenced, and within this region, 17 partial and complete open reading frames are present; all except one have sequence and positional homology to known gammaherpesvirus genes, including the major **capsid** protein and thymidine kinase genes.
Phylogenetic analyses using both single genes and combined gene sets demonstrated that the agent is a gamma-2 herpesvirus (genus Rhadinovirus) and is the first member of this genus known to infect humans. Evidence for transient viral transmission from infected to uninfected cells is presented, but replication-competent virions have not been identified in infected cell lines. Sera from patients with KS have specific antibodies directed against antigens of infected cell lines, and these antibodies are generally absent in sera from patients with AIDS without KS. These studies define the agent as a new human herpesvirus provisionally assigned the descriptive name KS-associated herpesvirus; its formal designation is likely to be human herpesvirus 8." The corresponding author for this study is: PS Moore, Columbia Univ, Div Epidemiol, P&s 14-442, 630 W 168TH St, New York, NY 10032 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 15 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 96:56340 PROMT

TITLE: Kaposi's Sarcoma Herpesvirus Moore, P.S.; Gao, S.J.; Dominguez, G.; Cesarman, E.; Lungu, O.; Knowles, D.M.; Garber, R.; Pellett, P.E.; Mcgeoch, D.J.; Chang, Y. "Primary Characterization of a Herpesvirus Agent Associated with Kaposi's sarcoma." Journal of Virology, January 1996;70(1):549-558.

SOURCE: Cancer Biotechnology Weekly, (29 Jan 1996) pp. N/A.

LANGUAGE: English

WORD COUNT: 296

FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB According to the authors' abstract of an article published in Journal of Virology, "Detection of novel DNA sequences in Kaposi's sarcoma (KS) and AIDS-related body cavity-based, non-Hodgkin's lymphomas suggests that these neoplasms are caused by a previously unidentified human herpesvirus. We have characterized this agent using a continuously infected B-lymphocyte cell line derived from an AIDS-related lymphoma and a genomic library made from a KS lesion, In this cell line, the agent has a large episomal genome with an electrophoretic mobility similar to that of 270-kb linear DNA markers during clamped homogeneous electric field gel electrophoresis. A 20.7-kb region of the genome has been completely sequenced, and within this region, 17 partial and complete open reading frames are present; all except one have sequence and positional homology to known gammaherpesvirus genes, including the major **capsid** protein and thymidine kinase genes.
Phylogenetic analyses using both single genes and combined gene sets demonstrated that the agent is a gamma-2 herpesvirus (genus Rhadinovirus) and is the first member of this genus known to infect humans. Evidence for transient viral transmission from infected to uninfected cells is presented, but replication-competent virions have not been identified in infected cell lines. Sera from patients with KS have specific antibodies directed against antigens of infected cell lines, and these antibodies are generally absent in sera from patients with AIDS without KS. These studies define the agent as a new human herpesvirus provisionally assigned the descriptive name KS-associated herpesvirus; its formal designation is likely to be human herpesvirus 8." The corresponding author for this study is: PS Moore, Columbia Univ, Div Epidemiol, P&s 14-442, 630 W 168TH St, New York, NY 10032 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 16 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 96:332442 PROMT
TITLE: Dengue Virus Bray, M.; Men, R.H.; Lai, C.J. "Monkeys Immunized with Intertypic Chimeric Dengue Viruses Are Protected Against Wild-Type Virus Challenge."
SOURCE: Vaccine Weekly, (24 Jun 1996) pp. N/A.
ISSN: 1074-2921.
LANGUAGE: English
WORD COUNT: 341
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Journal of Virology, June 1996;70(6):4162-4166.
According to the authors' abstract of an article published in Journal of Virology, "Dengue epidemics caused by the four dengue virus serotypes continue to pose a major public health problem in

most tropical and subtropical regions. A safe and effective vaccine against dengue is still not available. The current strategy for dengue immunization favors the use of a vaccine containing each of the four serotypes. We previously employed full-length dengue type 4 virus (DEN4) cDNA to construct a viable intertypic dengue virus of type 1 or type 2 antigenic specificity that contained the genes for the **capsid**-premembrane-envelope (C-pre-M-E) structural proteins of DEN1 or pre-M and E structural proteins of DEN2 substituting for the corresponding DEN4 genes. Chimeras DEN1/DEN4 and DEN2/DEN4, which express the nonstructural proteins of DEN4 and the C-pre-III-E structural proteins of DEN1 or the pre-hl-E structural proteins of DEN2, and therefore the antigenicity of type 1 or type 2, were used to immunize rhesus monkeys. Other monkeys were inoculated with parental DEN1, DEN2, or cDNA-derived DEN4. Three of four monkeys immunized with DEN1/DEN4 developed neutralizing antibodies against DEN1 and were protected against subsequent DEN1 challenge. All four monkeys immunized with DEN2/DEN4 developed antibodies against DEN2 and were protected against subsequent DEN2 challenge, DEN1- and DEN2-immunized monkeys were protected against homologous virus challenge, but DEN4-immunized animals became viremic on cross-challenge with DEN1 or DEN2. In a second experiment, eight monkeys were immunized with equal mixtures of DEN1/DEN4 and DEN2/DEN4. Each of these monkeys developed neutralizing antibodies against both DEN1 and DEN2 and were protected against subsequent challenge with DEN1 or DEN2. Chimeric dengue viruses similar to those described here could be used to express serotype-specific antigens in a live attenuated tetravalent human vaccine." The corresponding author for this study is: CJ Lai, Niaid, Mol Viral Biol Sect, Infect Dis Lab, 9000 Rockville Pike, Bethesda, MD 20892 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 17 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 96:339711 PROMT
TITLE: Dengue Virus "Monkeys Immunized with Intertypic Chimeric Dengue Viruses Are Protected Against Wild-Type Virus Challenge."
SOURCE: Blood Weekly, (24 Jun 1996) pp. N/A.
ISSN: 1065-6073.
LANGUAGE: English
WORD COUNT: 349
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Journal of Virology, June 1996;70(6):4162-4166.
Bray, M.; Men, R.H.; Lai, C.J.
According to the authors' abstract of an article published in Journal of Virology, "Dengue epidemics caused by the four dengue

virus serotypes continue to pose a major public health problem in most tropical and subtropical regions. A safe and effective vaccine against dengue is still not available. The current strategy for dengue immunization favors the use of a vaccine containing each of the four serotypes. We previously employed full-length dengue type 4 virus (DEN4) cDNA to construct a viable intertypic dengue virus of type 1 or type 2 antigenic specificity that contained the genes for the **capsid**-premembrane-envelope (C-pre-M-E) structural proteins of DEN1 or pre-M and E structural proteins of DEN2 substituting for the corresponding DEN4 genes. Chimeras DEN1/DEN4 and DEN2/DEN4, which express the nonstructural proteins of DEN4 and the C-pre-III-E structural proteins of DEN1 or the pre-hl-E structural proteins of DEN2, and therefore the antigenicity of type 1 or type 2, were used to immunize rhesus monkeys. Other monkeys were inoculated with parental DEN1, DEN2, or cDNA-derived DEN4. Three of four monkeys immunized with DEN1/DEN4 developed neutralizing antibodies against DEN1 and were protected against subsequent DEN1 challenge. All four monkeys immunized with DEN2/DEN4 developed antibodies against DEN2 and were protected against subsequent DEN2 challenge, DEN1- and DEN2-immunized monkeys were protected against homologous virus challenge, but DEN4-immunized animals became viremic on cross-challenge with DEN1 or DEN2. In a second experiment, eight monkeys were immunized with equal mixtures of DEN1/DEN4 and DEN2/DEN4. Each of these monkeys developed neutralizing antibodies against both DEN1 and DEN2 and were protected against subsequent challenge with DEN1 or DEN2. Chimeric dengue viruses similar to those described here could be used to express serotype-specific antigens in a live attenuated tetravalent human vaccine." The corresponding author for this study is: CJ Lai, Niaid, Mol Viral Biol Sect, Infect Dis Lab, 9000 Rockville Pike, Bethesda, MD 20892 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 18 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 95:162855 PROMT
TITLE: Papillomavirus - Virus-Cell Interactions Muller, M.; Gissmann, L.; Cristiano, R.J.; Sun, X.Y.; Frazer, I.H.; Jenson, A.B.; Alonso, A.; Zentgraf, H.; Zhou, J.A.
SOURCE: Cancer Biotechnology Weekly, (27 Feb 1995) pp. N/A.
LANGUAGE: English
WORD COUNT: 359
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB Journal of Virology, February 1995;69(2):948-954.
According to the authors' abstract of an article published in Journal of Virology, "The inability of papillomaviruses (PV) to

replicate in tissue culture cells has hampered the study of the PV life cycle. We investigated virus-cell interactions by the following two methods: (i) using purified bovine PV virions or human PV type 11 (HPV type 11) virus-like particles (VLP) to test the binding to eukaryotic cells and (ii) using different VLP -reporter plasmid complexes of HPV6b, HPV11 L1 or HPV11 L1/L2, and HPV16 L1 or HPV16 L1/L2 to study uptake of particles into different cell lines. Our studies showed that PV **capsids** bind to a broad range of cells in culture in a dose-dependent manner. Binding of PV **capsids** to cells can be blocked by pretreating the cells with the protease trypsin. Penetration of PV into cells was monitored by using complexes in which the purified PV **capsids** were physically linked to DNA containing the gene for beta-galactosidase driven by the human cytomegalovirus promoter. Expression of beta-galactosidase occurred in less than 1% of the cells, and the efficiency of PV receptor -mediated gene delivery was greatly enhanced (up to 10 to 20% positive cells) by the use of a replication-defective adenovirus which promotes endosomal lysis. The data generated by this approach further confirmed the results obtained from the binding assays, showing that PV enter a wide range of cells and that these cells have all functions required for the uptake of PV. Binding and uptake of PV particles can be blocked by PV-specific antisera, and different PV particles compete for particle uptake. Our results suggest that the PV receptor is a conserved cell surface molecule(s) used by different PV and that the tropism of infection by different PV is controlled by events downstream of the initial binding and uptake." The corresponding author for this study is: JA Zhou, Loyola Univ, Med Ctr, Dept Obstet & Gynecol, Div Res, Bldg 105, RM 2890, 2160 S 1ST Ave, Maywood, IL 60153 USA. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 19 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 94:310885 PROMT
TITLE: Andries, K.; Rombaut, B.; Dewindt, B.; Boeye, A. Poliovirus. Discrepancy Between Infectivity and Antigenicity Stabilization of Oral Poliovirus Vaccine by a Cap
SOURCE: Vaccine Weekly, (13 Jun 1994) pp. N/A.
ISSN: 1074-2921.
LANGUAGE: English
WORD COUNT: 213
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB SOURCE: Journal of Virology, May 1994;68(5):3397-3400.
According to the authors' abstract of an article published in the Journal of Virology, "Two hundred forty pyridazinamine derivatives

were tested for the ability to stabilize the antigenicity and infectivity of oral poliovirus vaccine subjected to 45deg.C for 2 h. Seven compounds stabilized the antigenicity of all three vaccine strains and neutralized the viral particles in a way that is reversible by dilution. Of these, R 77975 (pirodavir) was selected for vaccine potency tests. Sabin type 2 and type 3 strains were subjected to 4, 25, 42, and 45deg.C for 1 week in the presence and absence of R 77975. Although R 77975 particularly stabilized the infectivity of the most thermolabile vaccine strain (Sabin type 3), the protection did not exceed that of 1 M MgCl2. When virus was inactivated in the absence of R 77975, the native or N antigenicity changed in H antigenicity. However, in the presence of the **capsid** - binding compound, N antigenicity was preserved in particles that had lost infectivity." The corresponding author for this study is: K Andries, Janssen Res Fdn, Dept Virol, Turnhoutseweg 30, B-2340 Beerse, Belgium. For subscription information for this journal contact the publisher: Amer **Soc** Microbiology, 1325 Massachusetts Avenue, NW, Washington, DC 20005-4171.

L15 ANSWER 20 OF 39 PROMT COPYRIGHT 1999 IAC

ACCESSION NUMBER: 94:521953 PROMT
TITLE: Capsid Protein Virus-Like Particles Are Recognized
SOURCE: Cancer Researcher Weekly, (31 Oct 1994) pp. N/A.
ISSN: 1071-7226.
LANGUAGE: English
WORD COUNT: 186
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

AB by Neutralizing Monoclonal Antibodies and Induce High Titres of Neutralizing Antibodies." Journal of General Virology, September 1994;75(Part 9):2271 -2276.

According to the authors' abstract of an article published in the Journal of General Virology, "Baculovirus-expressed human papillomavirus type 11 (HPV -11) major **capsid** protein (L1) virus- like particles (VLPs) were produced in insect cells and purified on CsCl density gradients. The VLPs retained conformational neutralizing epitopes that were detected by a series of HPV -11- neutralizing monoclonal antibodies. Electron microscopy determined that the HPV-11 L1 VLPs were variable in size with a surface topography similar to that of infectious HPV-11. The VLPs were very antigenic, and induced high titres of neutralizing antibodies in rabbits and mice when used as an immunogen without commercial preparations of adjuvant. These VLP reagents may be effective vaccines for protection against HPV infections." The corresponding author for this study is: ND Christensen, Penn State Univ, Milton S Hershey Med Ctr, Dept Pathol, Hershey, PA 17033 USA. For subscription information for this journal contact the publisher:

Soc General Microbiology, Harvest House, 62 London Road, Reading RG1 5AS, United Kingdom.

L15 ANSWER 21 OF 39 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 93108451 MEDLINE
DOCUMENT NUMBER: 93108451
TITLE: Conformational changes of a viral **capsid** protein. Thermodynamic rationale for proteolytic regulation of bacteriophage T4 **capsid** expansion, co-operativity, and super-stabilization by **soc** binding.
AUTHOR: Steven A C; Greenstone H L; Booy F P; Black L W; Ross P D
CORPORATE SOURCE: Laboratory of Structural Biology, National Institute of Arthritis Musculoskeletal, and Skin Diseases, National Institutes of Health, Bethesda, MD 20892.
CONTRACT NUMBER: AI 11676 (NIAID)
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1992 Dec 5) 228 (3) 870-84.
Journal code: J6V. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
ENTRY MONTH: 199303

AB We have used differential scanning calorimetry in conjunction with cryo-electron microscopy to investigate the conformational transitions undergone by the maturing **capsid** of phage T4. Its precursor shell is composed primarily of gp23 (521 residues): cleavage of gp23 to gp23* (residues 66 to 521) facilitates a concerted conformational change in which the particle expands substantially, and is greatly stabilized. We have now characterized the intermediate states of **capsid** maturation; namely, the cleaved/unexpanded, state, which denatures at tm = 60 degrees C, and the uncleaved/expanded state, for which tm = 70 degrees C. When compared with the precursor uncleaved/unexpanded state (tm = 65 degrees C), and the mature cleaved/expanded state (tm = 83 degrees C, if complete cleavage precedes expansion), it follows that expansion of the cleaved precursor (delta tm approximately +23 degrees C) is the major stabilizing event in **capsid** maturation. These observations also suggest an advantage conferred by **capsid** protein cleavage (some other phage **capsids** expand without cleavage): if the gp23-delta domains (residues 1 to 65) are not removed by proteolysis, they impede formation of the stablest possible bonding arrangement when expansion occurs, most likely by becoming trapped at the interface between neighboring subunits or capsomers. Icosahedral **capsids** denature at essentially the same temperatures as

tubular polymorphic variants (polyheads) for the same state of the surface lattice. However, the thermal transitions of **capsids** are considerably sharper, i.e. more co-operative, than those of polyheads, which we attribute to **capsids** being closed, not open-ended. In both cases, binding of the accessory protein **soc** around the threefold sites on the outer surface of the expanded surface lattice results in a substantial further stabilization (delta tm = +5 degrees C). The interfaces between capsomers appear to be relatively weak points that are reinforced by clamp-like binding of **soc**. These results imply that the "triplex" proteins of other viruses (their structural counterparts of **soc**) are likely also to be involved in **capsid** stabilization. Cryo-electron microscopy was used to make conclusive interpretations of endotherms in terms of denaturation events. These data also revealed that the cleaved/unexpanded **capsid** has an angular polyhedral morphology and has a pronounced relief on its outer surface. Moreover, it is 14% smaller in linear dimensions than the cleaved/expanded **capsid**, and its shell is commensurately thicker.

L15 ANSWER 22 OF 39 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 93013031 MEDLINE
DOCUMENT NUMBER: 93013031
TITLE: Construction of a chimeric viral gene expressing plum pox virus coat protein.
AUTHOR: Ravelonandro M; Monsion M; Teycheney P Y; Delbos R; Dunez J
CORPORATE SOURCE: Station de Pathologie Vegetale, INRA, La Grande Ferrade, Villenave d'Ornon, France.
SOURCE: GENE, (1992 Oct 21) 120 (2) 167-73.
Journal code: FOP. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199301

AB The **capsid**-encoding gene of plum pox virus (PPV) was fused with the leader sequence of the coat protein mRNA (cp) of tobacco mosaic virus by a novel mutagenesis technique which involves reverse transcription of minus-strand RNA [synthesized by in vitro transcription of a double-stranded (ds) cDNA clone], using an ad **hoc** synthetic oligodeoxynucleotide as primer. The resulting cDNA was rendered ds and cloned into the plasmid, pBluescribe M13+. Transcription of this chimeric construction produced RNA molecules of 1250 nucleotides in length, which were used as messengers in the in vitro protein-synthesizing systems. The major product of this transcript consists of a 36-kDa polypeptide and was identified as the PPV coat protein (CP) by molecular weight estimation and by immunoprecipitation with a polyclonal antiserum to PPV. Transfer of

this cDNA via Agrobacterium tumefaciens into plants was successfully performed. Transgenic Nicotiana plants producing the PPV CP were subsequently obtained.

L15 ANSWER 23 OF 39 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 90255970 MEDLINE
DOCUMENT NUMBER: 90255970
TITLE: The bacteriophage T4 gene mrh whose product inhibits late T4 gene expression in an Escherichia coli rpoH (sigma 32) mutant.
AUTHOR: Frazier M W; Mosig G
CORPORATE SOURCE: Department of Molecular Biology, Vanderbilt University, Nashville, TN 37235..
CONTRACT NUMBER: GM13221 (NIGMS)
CA09385 (NCI)
SOURCE: GENE, (1990 Mar 30) 88 (1) 7-14.
Journal code: FOP. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M30001
ENTRY MONTH: 199008
AB In an Escherichia coli rpoH mutant (affecting sigma 32, heat-shock sigma factor) infected at high temperatures with wild-type T4 phage, late T4 transcription and consequently progeny production are dramatically impaired. This defect is due, in part, to insufficient activity of sigma 70 [Frazier and Mosig, J. Bacteriol. 170 (1988) 1384-1388], which is necessary to initiate early T4 transcription. Unexpectedly, however, we found that, in this rpoH host, late T4 transcription is also impaired when the temperature is raised from 30 to 42 degrees C late after infection, when T4 transcription is directed by the T4-encoded sigma factor, sigma gp55. Here, we show that a T4 gene that we call mrh (modulates rpoH), located at 14 kb on the T4 map, is responsible for the inhibition of late T4 transcription in the rpoH mutant host. T4 deletion mutants that lack the mrh gene can produce progeny in the rpoH host, but the Mrh protein, provided in trans from a plasmid-borne mrh gene, inhibits this growth. We have cloned and sequenced this T4 gene and synthesized the Mrh protein in a T7 RNA polymerase-dependent expression system. The Mr of the Mrh protein deduced from the nucleotide sequence is 13419. Gene mrh is cotranscribed with several other, yet unidentified genes, both from an early promoter downstream from the late **soc** gene (encoding the **small outer capsid** protein) and from the late **soc** promoter further upstream. (ABSTRACT TRUNCATED AT 250 WORDS)

L15 ANSWER 24 OF 39 MEDLINE DUPLICATE 10

ACCESSION NUMBER: 86037231 MEDLINE
DOCUMENT NUMBER: 86037231
TITLE: DNA packaging of bacteriophage T4 proheads in vitro. Evidence that prohead expansion is not coupled to DNA packaging.
AUTHOR: Rao V B; Black L W
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1985 Oct 5) 185 (3) 565-78.
Journal code: J6V. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
ENTRY MONTH: 198602

AB We developed a system for DNA packaging of isolated bacteriophage T4 proheads in vitro and studied the role of prohead expansion in DNA packaging. Biologically active proheads have been purified from a number of packaging-deficient mutant extracts. The cleaved mature prohead is the active structural precursor for the DNA packaging reaction. Packaging of proheads requires ATP, Mg2+ and spermidine, and is stimulated by polyethylene glycol and dextran. Predominantly expanded proheads (ELPs) are produced at 37 degrees C and predominantly unexpanded proheads (ESPs) are produced at 20 degrees C. Both the expanded and unexpanded proheads are active in DNA packaging in vitro. This is based on the observations that (1) both ESPs and ELPs purified by chromatography on DEAE-Sephacel showed DNA packaging activity; (2) apparently homogeneous ELPs prepared by treatment with sodium dodecyl sulfate (which dissociates ESPs) retained significant biological activity; (3) specific precipitation of ELPs with anti-**hoc** immunoglobulin G resulted in loss of DNA packaging activity; and (4) ESPs upon expansion in vitro to ELPs retained packaging activity. Therefore, contrary to the models that couple DNA packaging to head expansion, in T4 the expansion and packaging appear to be independent, since the already expanded DNA-free proheads can be packaged in vitro. We therefore propose that the unexpanded to expanded prohead transition has evolved to stabilize the **capsid** and to reorganize the prohead shell functionally from a core-interacting to a DNA-interacting inner surface.

L15 ANSWER 25 OF 39 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 85264792 MEDLINE
DOCUMENT NUMBER: 85264792
TITLE: Assembly-dependent conformational changes in a viral capsid protein. Calorimetric comparison of successive conformational states of the gp23 surface lattice of bacteriophage T4.
AUTHOR: Ross P D; Black L W; Bisher M E; Steven A C
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1985 Jun 5) 183 (3)

353-64.
Journal code: J6V. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
ENTRY MONTH: 198511

AB Inter- and intra-subunit bonding within the surface lattice of the **capsid** of bacteriophage T4 has been investigated by differential scanning calorimetry of polyheads, in conjunction with electron microscopy, limited proteolysis and sodium dodecyl sulfate/polyacrylamide gel electrophoresis. The bonding changes corresponding to successive stages of assembly of the major **capsid** protein gp23, including its maturation cleavage, were similarly characterized. The uncleaved/unexpanded surface lattice exhibits two endothermic transitions. The minor event, at 46 degrees C, does not visibly affect the surface lattice morphology and probably represents denaturation of the N-terminal domain of gp23. The major endotherm, at 65 degrees C, represents denaturation of the gp23 polymers. Soluble gp23 from dissociated polyheads is extremely unstable and exhibits no endotherm. Cleavage of gp23 to gp23* and the ensuing expansion transformation effects a major stabilization of the surface lattice of polyheads, with single endotherms whose melting temperatures (t*m) range from 73 to 81 degrees C, depending upon the mutant used and the fraction of gp23 that is cleaved to gp23* prior to expansion. Binding of the accessory proteins **soc** and **hoc** further modulates the thermograms of cleaved/expanded polyheads, and their effects are additive. **hoc** binding confers a new minor endotherm at 68 degrees C corresponding to at least partial denaturation of **hoc**. Denatured **hoc** nevertheless remains associated with the surface lattice, although in an altered, protease-sensitive state which correlates with delocalization of **hoc** subunits visualized in filtered images. While **hoc** binding has little effect on the thermal stability of the gp23* matrix, **soc** binding further stabilizes the surface lattice (delta Hd approximately +50%; delta t*m = +5.5 degrees C). It is remarkable that in all states of the surface lattice, the inter- and intra-subunit bonding configurations of gp23 appear to be co-ordinated to be of similar thermal stability. Thermodynamically, the expansion transformation is characterized by delta H much less than 0; delta Cp approximately 0, suggesting enhancement of van der Waals' and/or H-bonding interactions, together with an increased exposure to solvent of hydrophobic residues of gp23* in the expanded state. These findings illuminate hypotheses of **capsid** assembly based on conformational properties of gp23: inter alia, they indicate a role for the N-terminal portion of gp23 in regulating polymerization, and force a reappraisal of models of **capsid** swelling based on the swivelling of conserved

domains.

L15 ANSWER 26 OF 39 BIOSIS COPYRIGHT 1999 BIOSIS
ACCESSION NUMBER: 1985:296555 BIOSIS
DOCUMENT NUMBER: BA79:76551
TITLE: REGULATION OF A NEW BACTERIOPHAGE T-4 GENE 69 THAT SPANS AN ORIGIN OF DNA REPLICATION.
AUTHOR(S): MACDONALD P M; MOSIG G
CORPORATE SOURCE: DEP. BIOCHEM. MOL. BIOL., HARVARD UNIV., 7 DIVINITY AVE., CAMBRIDGE, MASS. 02138, USA.
SOURCE: EMBO (EUR MOL BIOL ORGAN) J, (1984) 3 (12), 2863-2872.
CODEN: EMJODG. ISSN: 0261-4189.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB The DNA sequence and transcription patterns was determined in a 3-kb [kilobase unit] segment (between 15 and 18 kb on the standard phage T4 map) spanning an origin of DNA replication. A new gene, 69, spans this origin. Gene 69 codes for 2 overlapping proteins that share a common C-terminal segment. Defective DNA replication in an appropriate amber mutant shows that at least the larger of the 2 proteins is required for efficient T4 DNA replication. The 2 proteins coded by gene 69 are expressed from different transcripts that are under different regulation. The smaller protein gp69*, can be expressed immediately from an Escherichia coli-like promoter, whereas expression of the larger protein, gp69, must be delayed since its middle promoter requires T4 coded protein, most likely gp mot, for activation. The possible significance was discussed of 2 overlapping proteins in the assembly of replisomes. Gene 69 is bracketed by the nonessential early gene dam (DNA adenine methylase) and late gene **soc** (**small outer capsid** protein). Transcripts through this region are interdigitated in a complex pattern, which reveals all elements that are thought to be important in regulation of pre-replicative and post-replicative T4 genes.

L15 ANSWER 27 OF 39 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 85070957 MEDLINE
DOCUMENT NUMBER: 85070957
TITLE: Infection of neuronal cell cultures with reovirus mimics in vitro patterns of neurotropism.
AUTHOR: Dichter M A; Weiner H L
CONTRACT NUMBER: NS-16998 (NINDS)
SOURCE: ANNALS OF NEUROLOGY, (1984 Nov) 16 (5) 603-10.
Journal code: 6AE. ISSN: 0364-5134.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 198503
AB Primary neuronal cell cultures of rat fetal cerebral cortex serve as in vitro models for the study of a variety of neuronal membrane receptors. Such studies have focused primarily on receptors for neurotransmitters and drugs. In the present series of experiments, we have employed this model to study the in vitro pattern of infection with reovirus types 1 and 3, two well-characterized neurotropic viruses that show specificity for neurons (type 3) or ependymal cells (type 1) in vivo and whose specificity has been linked with surface receptors on somatic cells. We have found that in primary neural cell culture, reovirus type 3 maintained its specificity by infecting neurons whereas reovirus type 1 did not infect neurons. Both serotypes infected astrocytes in the cultures, type 1 to a greater extent than type 3. In addition, reovirus type 3 bound to the surface of neurons whereas type 1 did not. Using recombinant viral clones, the in vitro tropism and the neuronal binding were shown to be properties of the viral hemagglutinin, a **small outer capsid** viral protein, as is the case with the neurotropism in vivo. It is postulated that the neurotropism of reovirus type 3 is related to the interaction of the viral hemagglutinin with an as yet undefined structure on the neuronal surface.

L15 ANSWER 28 OF 39 MEDLINE DUPLICATE 13
ACCESSION NUMBER: 83189364 MEDLINE
DOCUMENT NUMBER: 83189364
TITLE: Evidence that bacteriophage T4 eph1 is a missense hoc mutation.
AUTHOR: Childs J D; Pilon R
SOURCE: JOURNAL OF VIROLOGY, (1983 May) 46 (2) 629-31.
Journal code: KCV. ISSN: 0022-538X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
ENTRY MONTH: 198308
AB An electrophoretic mutation of bacteriophage T4, eph1, appears to code for a missense **hoc** (**highly** antigenic **outer capsid**) protein. This is based on the observation that particles lacking **hoc** protein (**hoc**- particles), after incubation in a crude extract of Escherichia coli infected with phage carrying the eph1 mutation acquired the electrophoretic mobility of the eph1 strain (the electrophoretic mobility of the eph1 strain itself is slower than that of **hoc**- particles). Thus, it is likely that during infection of E. coli with the eph1 strain, a **hoc** protein is made that has a lower negative charge than normal **hoc** protein but can nevertheless bind to particles lacking **hoc** protein. These results confirm that eph1 is a **hoc**

mutation.

L15 ANSWER 29 OF 39 BIOSIS COPYRIGHT 1999 BIOSIS
ACCESSION NUMBER: 1983:196223 BIOSIS
DOCUMENT NUMBER: BA75:46223
TITLE: AVIAN REOVIRUS POLY PEPTIDES ANALYSIS OF INTRA CELLULAR VIRUS SPECIFIED PRODUCTS VIRIONS TOP COMPONENT AND CORES.
AUTHOR(S): SCHNITZER T J; RAMOS T; GOUVEA V
CORPORATE SOURCE: RACKHAM ARTHRITIS RESEARCH UNIT, DEPARTMENT OF INTERNAL MEDICINE, SCHOOL OF MEDICINE, UNIVERSITY OF MICHIGAN, ANN ARBOR, MICHIGAN 48109.
SOURCE: J VIROL, (1982) 43 (3), 1006-1014.
CODEN: JOVIAM. ISSN: 0022-538X.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Avian reovirus-specified polypeptides can be separated into 3 size large (.lambda.), medium (.mu.) and small (.sigma.), similar to those of the mammalian reoviruses. A nomenclature has been proposed to indicate the individual polypeptides within each size class by progressive alphabetical subscripts. Three .lambda. polypeptides (.lambda.A, .lambda.B and .lambda.C) are found in infectious viral particles and have MW of 145,000, 130,000 and 115,000, respectively. All are present in core preparations, and 2 (.lambda.A and .lambda.B) appear to be exposed at the surface of the virion. Two .mu. polypeptides can be distinguished in purified virus (.mu.A, 72,000 daltons (72 kd); .mu.B 70 kd), and another is occasionally evident by immunoprecipitation from infected chicken embryo fibroblast cell extracts (.mu.NS). .mu.B represents the major outer capsid protein and is structurally homologous to .mu.1C of the mammalian reoviruses. No additional .mu. proteins can be detected, and there is no evidence for a product-precursor relationship among these proteins. Three major .sigma. proteins are evident in viral particles. .sigma.C has the lowest MW, is part of the outer capsid of the virion and appears homologous to the mammalian .sigma.1 protein. It demonstrates the greatest polymorphism of all the polypeptides among the different avian reoviruses examined. .sigma.B (36 kid) is a major constituent of the outer capsid and, like .sigma.C, is exposed to the surface of the virion. .sigma.A (39 kd) appears to be an internal protein. An additional polypeptide band in the .sigma. class having an apparent MW of 34,000 to 35,000 can be seen under 3 different conditions: in some S1133 reovirus preparations, particularly after prolonged storage, a new band (.sigma.B') appears with a reduction in intensity of .sigma.B, suggesting that .sigma.B' is a degradation product of .sigma.B; in polypeptides immunoprecipitated from infected cell extracts, a major band (.sigma.NS) is apparent migrating just ahead of .sigma.B; (iii) in top component preparations from all avian reoviruses examined, a band (.sigma.TC) with mobility identical to that of .sigma.NS

represents a major constituent and appears to be incorporated within the particle itself. The relationship among these 3 bands is not currently known. Avian reovirus polypeptides are thus in general similar to those found in mammalian reoviruses, but differences do exist which may be important for understanding viral structure and assembly.

L15 ANSWER 30 OF 39 BIOSIS COPYRIGHT 1999 BIOSIS
ACCESSION NUMBER: 1980:283122 BIOSIS
DOCUMENT NUMBER: BA70:75618
TITLE: HEAD SHELL PROTEIN HOC ALTERS THE SURFACE CHARGE OF BACTERIO PHAGE T-4 COMPOSITE SLAB GEL ELECTROPHORESIS OF PHAGE T-4 AND RELATED PARTICLES.
AUTHOR(S): YAMAGUCHI Y; YANAGIDA M
CORPORATE SOURCE: DEP. BIOPHYS., FAC. SCI., KYOTO UNIV., SAKYO, KYOTO 606, JPN.
SOURCE: J MOL BIOL, (1980) 141 (2), 175-194.
CODEN: JMOBAK. ISSN: 0022-2836.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Agarose/polyacrylamide gel electrophoresis was used to separate bacteriophages and related particles. A T4 mutant T4 **hoc**, wild-type T2, T6 and RB69, all of which lack one of the non-essential head shell proteins, **hoc** (**highly** antigenic **outer capsid** protein), migrated at much faster rates to the anode at pH 8.3, compared to T4 **hoc** + and other RB phage strains. The mobility difference between **hoc**+ and **hoc**- phage phage appears to be due primarily to a net charge difference, and is neither caused by any particle weight difference nor by any difference in the shape of the phages. The isolated **hoc** protein is capable of binding to T4 **hoc** particles, and the binding reaction could be followed by composite gel electrophoresis. A single electrophoretic band of partially reconstituted T4 **hoc** phages with a mobility intermediate between **hoc** and **hoc**+ phages supports a non-co-operative binding model. The binding velocity V was proportional to the **hoc** concentration, [**hoc**], and the ratio, f, of the unbound to the total number of binding sites. T4 **hoc** phage particles aggregate at low ionic strength to form large clumps. The aggregation is reversible and inhibited by addition of divalent cations such as Mg2+ or Ca2+. The **hoc** protein may be involved in keeping the interaction between phages to a minimum. The electrophoretic properties of the structural parts of phage T4, various bacteriophages and protein assemblies are described. The composite gel system is useful for studies on viruses and supramolecules.

L15 ANSWER 31 OF 39 BIOSIS COPYRIGHT 1999 BIOSIS
ACCESSION NUMBER: 1980:283121 BIOSIS

DOCUMENT NUMBER: BA70:75617
TITLE: EFFECT OF HOC PROTEIN ON THE ELECTROPHORETIC MOBILITY OF INTACT BACTERIO PHAGE T-4D PARTICLES IN POLY ACRYLAMIDE GEL ELECTROPHORESIS.
AUTHOR(S): CHILDS J D
CORPORATE SOURCE: RADIAT. BIOL. BRANCH, AT. ENERGY CAN. LTD., CHALK RIVER, ONT. KOJ 1J0, CAN.
SOURCE: J MOL BIOL, (1980) 141 (2), 163-174.
CODEN: JMOBAK. ISSN: 0022-2836.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB The electrophoretic mobility of intact bacteriophage T4D particles lacking a nonessential head protein, **hoc**, was 24% faster than wild-type particles in 1.85% polyacrylamide gels at pH 8.3. Another nonessential outer **capsid** protein, **soc**, did not appear to influence the electrophoretic mobility of phage particles either in the presence or absence of **hoc** protein. A previously isolated electrophoretic mutant, eph1, which migrated 14% more slowly than wild type, has immunologically detectable **hoc** protein. This mutant, like **hoc**, appears to affect electrophoretic mobility by changing the net charge of the phage particles. Both eph1 and **hoc** are located between genes 24 and 25 adjacent to a continuous sequence of head assembly genes (genes 20 to 24). Particles from a mixed infection of eph1 and eph+ migrated as a diffuse band with a mobility intermediate between eph1 and eph+. This indicates that phenotypic mixing had probably occurred with the production of hybrid phage particles containing random amounts of mutant and normal eph protein. Complementation tests based on phenotypic mixing rules out the possibility that the eph1 mutation is in genes 24 and 25 and showed that it is probably a missense **hoc** mutant.

L15 ANSWER 32 OF 39 BIOSIS COPYRIGHT 1999 BIOSIS
ACCESSION NUMBER: 1978:218538 BIOSIS
DOCUMENT NUMBER: BA66:31035
TITLE: BINDING OF THE STRUCTURAL PROTEIN SOC TO THE HEAD SHELL OF BACTERIO PHAGE T-4.
AUTHOR(S): ISHII T; YAMAGUCHI Y; YANAGIDA M
CORPORATE SOURCE: DEP. BIOPHYS., FAC. SCI., KYOTO UNIV., SAKYO, KYOTO, JPN.
SOURCE: J MOL BIOL, (1978) 120 (4), 533-544.
CODEN: JMOBAK. ISSN: 0022-2836.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Kinetic experiments on the binding reaction of the **small outer capsid** protein **soc** to the head shell of bacteriophage T4 are presented. The relationship between the binding velocity V, the **soc** concentration and the ratio f of unoccupied to the total number of binding sites is

approximately V .infin. [**soc**]1.4 .times. f2.2 at 37.degree. C: the rate of binding decreases sharply as the reaction proceeds. The reaction is rather complex, interpreted either as the binding to the sites of different affinity for **soc** or as negatively concerted binding. The **highly** antigenic **outer capsid** protein **hoc** seems to bind to identical and independent binding sites, because the relation V .infin. [**hoc**] .times. f was obtained. Using the double mutant T4soc **hoc** showed that **soc** and **hoc** binding are mutually independent, at least under the experimental conditions used here.

L15 ANSWER 33 OF 39 MEDLINE DUPLICATE 14
ACCESSION NUMBER: 78197066 MEDLINE
DOCUMENT NUMBER: 78197066
TITLE: Head maturation pathway of bacteriophages T4 and T2. IV. In vitro transformation of T4 head-related particles produced by mutants in gene 17 to capsid-like structures.
AUTHOR: Carrascosa J L
SOURCE: JOURNAL OF VIROLOGY, (1978 May) 26 (2) 420-8. Journal code: KCV. ISSN: 0022-538X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197810
AB T4 mutants in gene 17 accumulate particles which contain the main head protein in the cleaved form (gp23*) arranged in an unexpanded lattice (empty small particles), together with other expanded **capsids** (empty large particles). The isolated empty small particles can be transformed in vitro, by lowering the ionic strength, to **capsid**-like structures. This structural transformaton is not coupled to chemical modification of the structural proteins of the empty small particles. In contrast to unexpanded particles that are easily dissociated, the transformed structures are as resistant to dissociation as other T-even head-related particles with expanded lattice. Furthermore, the transformed particles are able to bind in vitro **hoc** and **soc** proteins, rendering **capsids** indistinguishable from the normal T4 **capsids** both morphologically and by their stability against denaturing agents. Our results indicate that the in vitro transformation of the empty small particles might mimic important and characteristic aspects of the in vivo maturation of T4 heads, thus suggesting a possible role of the "cleaved but unexpanded" particle in the maturation pathway of the T4 shell.

L15 ANSWER 34 OF 39 MEDLINE DUPLICATE 15
ACCESSION NUMBER: 79007647 MEDLINE

DOCUMENT NUMBER: 79007647
TITLE: Isolation and characterization of bacteriophage T4 mutant preheads.
AUTHOR: Onorato L; Stirmer B; Showe M K
SOURCE: JOURNAL OF VIROLOGY, (1978 Aug) 27 (2) 409-26.
Journal code: KCV. ISSN: 0022-538X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197901

AB To determine the function of individual gene products in the assembly and maturation of the T4 prehead, we have isolated and characterized aberrant preheads produced by mutations in three of the T4 head genes. Mutants in gene 21, which codes for the T4 maturation proteases, produce rather stable preheads whose morphology and protein composition are consistent with a wild-type prehead blocked in the maturation cleavages. Mutants in gene 24 produce similar structures which are unstable because they have gaps at all of their icosahedral vertices except the membrane attachment site. In addition, greatly elongated "giant preheads" are produced, suggesting that in the absence of P24 at the vertices, the distal cap of the prehead is unstable, allowing abnormal elongation of broth the prehead core and its shell. Vertex completion by P24 is required to allow the maturation cleavages to occur, and 24- preheads can be matured to **capsids** in vitro by the addition of P24. Preheads produced by a temperature-sensitive mutant in gene 23 are deficient in core proteins. We show that the shell of these preheads has the expanded lattice characteristic of the mature **capsid** as well as the binding sites for the proteins **hoc** and **soc**, even though none of the maturation cleavage takes place. We also show that 21- preheads composed of wild-type P23 can be expanded in vitro without cleavage.

L15 ANSWER 35 OF 39 MEDLINE DUPLICATE 16
ACCESSION NUMBER: 78153769 MEDLINE
DOCUMENT NUMBER: 78153769
TITLE: Complete primary structure of the **small outer capsid (soc)** protein of bacteriophage T4.
AUTHOR: Bijlenga R K; Ishii T; Tsugita A
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1978 Apr 5) 120 (2) 249-63.
Journal code: J6V. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197808

L15 ANSWER 36 OF 39 BIOSIS COPYRIGHT 1999 BIOSIS DUPLICATE 17
ACCESSION NUMBER: 1977:219901 BIOSIS
DOCUMENT NUMBER: BA64:42265
TITLE: CAPSID FINE STRUCTURE OF T EVEN BACTERIO PHAGES BINDING AND LOCALIZATION OF 2 DISPENSABLE CAPSID PROTEINS INTO THE P-23 SURFACE LATTICE.
AUTHOR(S): AEBI U; VAN DRIEL R; BIJLENGA R K L; TEN HEGGELER B; VAN DEN BROEK R; STEVEN A C; SMITH P R
SOURCE: J MOL BIOL, (1977) 110 (4), 687-698.
CODEN: JMOBAK. ISSN: 0022-2836.
FILE SEGMENT: BA; OLD
LANGUAGE: Unavailable
AB Two methods were used to identify the stain-excluding regions in the P23* matrix of the T-even phage **capsid**, and to investigate the bonding of the dispensable proteins **hoc** and **soc** into this matrix. T2L giant phage **capsids** which lack **hoc** and **soc** were titrated with these 2 proteins. The **hoc**, **soc** and other **capsid** proteins were differentially dissociated from T4D and from **hoc** and **soc** complemented T2L **capsids** by reversible acylation with citraconic anhydride. Changes in the capsomeres of giant **capsids** were monitored by EM followed by optical filtration of the electron micrographs. The stain-excluding region in the center of the capsomere is apparently associated with binding of 1 molecule of **hoc** protein, and the 6 stain-excluding regions bridging adjacent capsomeres are associated with the binding of 6 molecules of **soc** protein. The binding of **soc** in the absence of **hoc** is highly co-operative, but the presence of **hoc** in the P23* lattice induces a marked heterogeneity in the **soc** binding sites.

L15 ANSWER 37 OF 39 EMBASE COPYRIGHT 1999 ELSEVIER SCI. B.V.DUPLICATE 18
ACCESSION NUMBER: 78032726 EMBASE
DOCUMENT NUMBER: 1978032726
TITLE: The two dispensable structural proteins (**soc** and **hoc**) of the T4 phage **capsid**; their purification and properties, isolation and characterization of the defective mutants, and their binding with the defective heads in vitro.
AUTHOR: Ishii T.; Yanagida M.
CORPORATE SOURCE: Dept. Biophys., Fac. Sci., Kyoto Univ., Kyoto, Japan
SOURCE: Journal of Molecular Biology, (1977) 109/4 (487-514).
CODEN: JMOBAK
DOCUMENT TYPE: Journal
FILE SEGMENT: 029 Clinical Biochemistry
004 Microbiology
Searcher : Shears 308-4994

047 Virology
LANGUAGE: English

L15 ANSWER 38 OF 39 MEDLINE DUPLICATE 19
ACCESSION NUMBER: 77211099 MEDLINE
DOCUMENT NUMBER: 77211099
TITLE: Comparison of the structural and chemical composition of giant T-even phage heads.
AUTHOR: Aebi U; Bijlenga R K; ten Heggeler B; Kistler J; Steven A C; Smith P R
SOURCE: JOURNAL OF SUPRAMOLECULAR STRUCTURE, (1976) 5 (4) 475-95.
Journal code: K75. ISSN: 0091-7419.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197710
AB A study has been made of the structure of the **capsids** of T4D giant phage produced from mutants in gene 23 and temperature-sensitive mutants in gene 24, and T4D and T2L giant phage formed by the addition of L-canavanine followed by an Larginine chase in the growth medium. All the giant phage **capsids** have been shown to be built according to the same geometrical architecture. This consists of a near-hexagonal surface net, lattice constant 129.5 A, folded into a left-handed T = 13 prolate icosahedron elongated along one of its fivefold symmetry axes. Their only apparent difference from wild-type T-even phage **capsids** is their abnormally elongated tubular part. A comparison of the capsomere morphologies and protein compositions of the giant phage **capsids** showed that all T4D giants are identical but differ from T2L: The T4D capsomere has a complex (6 + 6 + 1)-type morphology, whereas the T2L has a simple 6-type. T2L phage, however, lack two **capsid** proteins, "**soc**" and "**hoc**", present in T4D. The difference in capsomere morphology can therefore be related to the difference in the protein compositions of these two phage. Possible differences between the initiation and means of length regulation of giant phage heads and the aberrant polyheads are discussed.

L15 ANSWER 39 OF 39 BIOSIS COPYRIGHT 1999 BIOSIS DUPLICATE 20
ACCESSION NUMBER: 1977:111155 BIOSIS
DOCUMENT NUMBER: BA63:6019
TITLE: STRUCTURE OF PHAGE T-4 POLY HEADS PART 2 A PATHWAY OF POLY HEAD TRANSFORMATIONS AS A MODEL FOR PHAGE T-4 CAPSID MATURATION.
AUTHOR(S): STEVEN A C; COUTURE E; AEBI U; SHOWE M K
SOURCE: J MOL BIOL, (1976) 106 (1), 187-221.
CODEN: JMOBAK. ISSN: 0022-2836.

FILE SEGMENT: BA; OLD
LANGUAGE: Unavailable
AB The aberrant tubular polyheads of bacteriophages T4D and T2L were studied as a model system for **capsid** maturation. Six different types of polyhead surface lattice morphology, and the corresponding protein compositions are discussed. Using in vitro systems to induce transformations between particular polyhead types, it was deduced that the structural classes represent successive points in a transitional pathway. In the 1st step, coarse polyheads (analogous to the prohead .tau.-particle) are proteolytically cleaved by a phage-coded protease, a fragment of the gene 21 product. This cleavage of P23 to P23* induces a co-operative lattice transformation in the protein of the surface shell, to a conformation equivalent to that of T2L giant phage **capsids** . These polyheads (derived either from T4 or T2L lysates) can accept further T4-coded proteins. In doing so, they pass through intermediate structural states, eventually reaching an end point whose unit cell morphology is indistinguishable from that of the giant T4 **capsids**. At least 1 protein (called **soc** (Ishii & Yanagida, 1975)) is bound stoichiometrically to P23* in the end-state conformation. The simulation of several aspects of **capsid** maturation (cleavage of P23 to P23*, stabilization and lattice expansion) in the polyhead pathway suggest that it parallels the major events of phage T-even **capsid** maturation, decoupled from any involvement of DNA packaging.

=> d his l16-; d 1-20 ibib abs

(FILE 'CAPLUS, MEDLINE, BIOSIS, EMBASE, LIFESCI, BIOTECHDS, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, PROMT' ENTERED AT 16:16:11 ON 02 AUG 1999)

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L16          806 S STEVEN A?/AU
L17          733 S WINGFIELD P?/AU
L18         1706 S BLACK L?/AU
L19            0 S ZHAOJUN R?/AU
L20            7 S L16 AND L17 AND L18
L21          102 S L16 AND (L17 OR L18)
L22            7 S L17 AND L18
L23           80 S L21 AND (SOC OR HOC OR CAPSID)
L24           80 S L20 OR L22 OR L23
L25           20 DUP REM L24 (60 DUPLICATES REMOVED)
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+ Author(s)

L25 ANSWER 1 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 1
ACCESSION NUMBER: 1999:283919 CAPLUS
DOCUMENT NUMBER: 131:69967
TITLE: Separation and crystallization of T = 3 and T = 4 icosahedral complexes of the hepatitis B virus core protein
AUTHOR(S): Zlotnick, Adam; Palmer, Ira; Kaufman, Joshua D.;

Searcher : Shears 308-4994

Stahl, Stephen J.; **Steven, Alasdair C.** ; **Wingfield, Paul T.**
CORPORATE SOURCE: Protein Expression Laboratory, National Institute of Arthritis, Musculoskeletal and Skin Diseases, National Institutes of Health, Bethesda, MD, 20892, USA
SOURCE: Acta Crystallogr., Sect. D: Biol. Crystallogr. (1999), D55(3), 717-720
CODEN: ABCRE6; ISSN: 0907-4449
PUBLISHER: Munksgaard International Publishers Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The icosahedral nucleocapsid of human hepatitis B virus is a homopolymer of the dimeric **capsid** protein also known as hepatitis B core antigen or HBcAg. Purified **capsid** protein obtained from an Escherichia coli expression system was reassembled into a mixt. of T = 3 and T = 4 icosahedral particles consisting of 90 and 120 dimers, resp. The two types of **capsid** were sepd. on a preparative scale by centrifugation through a sucrose gradient. In addn. to this heterogeneity, the **capsid** protein has three cysteines, one of which has a great propensity for forming disulfide bonds between the two subunits, forming a dimer. To eliminate heterogeneity arising from oxidn., alanines were substituted for the cysteines. T = 3 and T = 4 **capsids** crystd. under similar conditions. Crystals of T = 3 **capsids** diffracted to .apprx.8 .ANG. resoln.; crystals of T = 4 **capsids** diffracted to 4 .ANG. resoln.

L25 ANSWER 2 OF 20 BIOSIS COPYRIGHT 1999 BIOSIS
ACCESSION NUMBER: 1999:186606 BIOSIS
DOCUMENT NUMBER: PREV199900186606
TITLE: Mapping sites on the surface of the hepatitis B virus **capsid** by cryo-electron microscopy with tetra-iridium clusters.
AUTHOR(S): Cheng, N. (1); Conway, J. F. (1); Watts, N. (1); Hainfeld, J. F.; Powell, R. D.; Joshi, V.; Stahl, S. J. (1); **Wingfield, P. T. (1)**; **Steven, A. C. (1)**
CORPORATE SOURCE: (1) NIAMS-NIH, Bethesda, MD, 20892 USA
SOURCE: Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2, pp. A457.
Meeting Info.: Forty-third Annual Meeting of the Biophysical Society Baltimore, Maryland, USA February 13-17, 1999
ISSN: 0006-3495.
DOCUMENT TYPE: Conference
LANGUAGE: English

L25 ANSWER 3 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 2

ACCESSION NUMBER: 1998:805545 CAPLUS
DOCUMENT NUMBER: 130:135593
TITLE: Localization of the N terminus of hepatitis B virus **capsid** protein by peptide-based difference mapping from cryoelectron microscopy
AUTHOR(S): Conway, J. F.; Cheng, N.; Zlotnick, A.; Stahl, S. J.; **Wingfield, P. T.**; **Steven, A. C.**
CORPORATE SOURCE: Laboratory of Structural Biology Research, National Institute of Arthritis, Musculoskeletal and Skin Diseases, National Institutes of Health, Bethesda, MD, 20892, USA
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1998), 95(25), 14622-14627
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Recently, cryoelectron microscopy of isolated macromol. complexes has advanced to resolns. below 10 .ANG., enabling direct visualization of .alpha.-helical secondary structure. To help correlate such d. maps with the amino acid sequences of the component proteins, we advocate peptide-based difference mapping, i.e., insertion of peptides, .apprxeq. 10 residues long, at targeted points in the sequence and visualization of these peptides as bulk labels in cryoelectron microscopy-derived difference maps. As proof of principle, we have appended an extraneous octapeptide at the N terminus of hepatitis B virus **capsid** protein and detd. its location on the **capsid** surface by difference imaging at 11 .ANG. resoln. Hepatitis B virus **capsids** are icosahedral particles, .apprxeq.300 .ANG. in diam., made up of T-shaped dimers (subunit Mr, 16-21 kDa, depending on construct). The stems of the Ts protrude outward as spikes, whereas the crosspieces pack to form the contiguous shell. The two N termini per dimer reside on either side of the spike-stem, at the level at which it enters the shell. This location is consistent with formation of the known intramol. disulfide bond between the cysteines at positions 61 and - 7 (in the residual propeptide) in the "e-antigen" form of the **capsid** protein and has implications for why this clin. important antigen remains unassembled in vivo.

L25 ANSWER 4 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 3
ACCESSION NUMBER: 1998:432010 CAPLUS
DOCUMENT NUMBER: 129:172983
TITLE: Hepatitis B virus **capsid**: localization of the putative immunodominant loop (residues 78 to 83) on the **capsid** surface, and implications for the distinction between c and e-antigens

Searcher : Shears 308-4994

AUTHOR(S): Conway, J. F.; Cheng, N.; Zlotnick, A.; Stahl, S. J.; **Wingfield, P. T.**; Belnap, D. M.; Kanngiesser, U.; Noah, M.; **Steven, A. C.**

CORPORATE SOURCE: Lab. Structural Biol. Res., Natl. Institutes of Health, Bethesda, MD, 20892, USA

SOURCE: J. Mol. Biol. (1998), 279(5), 1111-1121
CODEN: JMOBAK; ISSN: 0022-2836
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Hepatitis B virus **capsid** protein comprises a 149 residue "assembly" domain that polymerizes into icosahedral particles, and a 34 residue RNA-binding "protamine" domain. Recently, the **capsid** structure has been studied to resolns. below 10 .ANG. by cryo-electron microscopy, revealing much of its .alpha.-helical substructure and that it appears to have a novel fold for a **capsid** protein; however, the resoln. is still too low for chain-tracing by conventional criteria. Aiming to establish a fiducial marker to aid in the process of chain-tracing, the authors have used cryo-microscopy to pinpoint the binding site of a monoclonal antibody that recognizes the peptide from residues 78 to 83. This epitope resides on the outer rim of the 30 .ANG. long spikes that protrude from the **capsid** shell. These spikes are four-helix bundles formed by the pairing of helix-turn-helix motifs from two subunits; by a tilting expt., the authors have detd. that this bundle is right-handed. Variants of the same protein present two clin. important and non-crossreactive antigens: core antigen (HBcAg), which appears early in infection as assembled **capsids**; and the sentinel e-antigen (HBeAg), a non-particulate form. Knowledge of the binding site of the authors' anti-HBcAg antibody bears on the mol. basis of the distinction between the assembled and unassembled states of **capsid** protein dimer, in addn. to epitope masking in **capsids**.

L25 ANSWER 5 OF 20 CAPLUS COPYRIGHT 1999 ACS

ACCESSION NUMBER: 1998:737865 CAPLUS

DOCUMENT NUMBER: 130:136088

TITLE: Mapping protein folds in "single particle" density maps from cryo-electron microscopy at 8 - 10 .ANG. resolution

AUTHOR(S): **Steven, A. C.**; Conway, J. F.; Cheng, N.; Zlotnick, A.; Stahl, S. J.; **Wingfield, P. T.**

CORPORATE SOURCE: NIAMS, National Institutes of Health, Bethesda, MD, 20892, USA

SOURCE: Electron Microsc. 1998, Proc. Int. Congr., 14th (1998), Volume 1, 727-728. Editor(s): Calderon

Searcher : Shears 308-4994

Benavides, Hector A.; Jose Yacaman, Miguel.
Institute of Physics Publishing: Bristol, UK.
CODEN: 66YYA4
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The resoln. attained in cryo-electron microscopy analyses of single particles (large sets of identical free-standing particles) has advanced significantly. In studies of the hepatitis B virus **capsid**, now at 8.ANG. resoln., the authors explored several approaches aimed at identifying the exact locations of designated amino acids or peptides in the d. map.

L25 ANSWER 6 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 4
ACCESSION NUMBER: 1998:511821 CAPLUS
DOCUMENT NUMBER: 129:227877
TITLE: Shared motifs of the **capsid** proteins of hepadnaviruses and retroviruses suggest a common evolutionary origin
AUTHOR(S): Zlotnick, Adam; Stahl, Steven J.; **Wingfield, Paul T.**; Conway, James F.; Cheng, Naiqian; **Steven, Alasdair C.**
CORPORATE SOURCE: Protein Expression Laboratory, NIAMS-NIH, Bethesda, MD, 20892-2717, USA
SOURCE: FEBS Lett. (1998), 431(3), 301-304
CODEN: FEBLAL; ISSN: 0014-5793
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The structure of the dimeric C-terminal domain of the HIV-1 **capsid** protein (CA), recently detd. by X-ray crystallog. (Gamble et al. (1997)), has a notable resemblance to the structure of the hepatitis B virus (HBV) **capsid** protein (Cp) dimer, previously detd. by cryo-electron microscopy (Conway et al. (1997), Bottcher et al. (1997)). In both proteins, dimerization is effected by formation of a four-helix bundle, whereby each subunit contributes a helix-loop-helix and most of the interaction between subunits is mediated by one pair of helixes. These are the first two observations of a motif that is common to the **capsid** proteins of two enveloped viruses and quite distinct from the eight-stranded anti-parallel .beta.-barrel found in most other virus **capsid** proteins solved to date (Harrison et al. (1996)). Motivated by the structural resemblance, we have examd. retroviral and HBV **capsid** protein sequences and found weak but significant similarities between them. These similarities further support an evolutionary relationship between these two virus families of great medical importance - the hepadnaviruses (e.g. HBV) and retroviruses (e.g. HIV).

L25 ANSWER 7 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 5

ACCESSION NUMBER: 1997:580873 CAPLUS
DOCUMENT NUMBER: 127:259842
TITLE: Localization of the C terminus of the assembly domain of hepatitis B virus **capsid** protein: implications for morphogenesis and organization of encapsidated RNA
AUTHOR(S): Zlotnick, A.; Cheng, N.; Stahl, S. J.; Conway, J. F.; **Steven, A. C.**; **Wingfield, P. T.**
CORPORATE SOURCE: National Institute of Arthritis, Musculoskeletal and Skin Diseases, National Institutes of Health, Bethesda, MD, 20892, USA
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1997), 94(18), 9556-9561
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The **capsid** protein of hepatitis B virus, consisting of an "assembly" domain (residues 1-149) and an RNA-binding "protamine" domain (residues 150-183), assembles from dimers into icosahedral **capsids** of two different sizes. The C terminus of the assembly domain (residues 140-149) functions as a morphogenetic switch, longer C termini favoring a higher proportion of the larger **capsids**; it also connects the protamine domain to the **capsid** shell. We now have defined the location of this peptide in **capsids** assembled in vitro by engineering a mutant assembly domain with a single cysteine at its C terminus (residue 150), labeling it with a gold cluster and visualizing the cluster by cryoelectron microscopy. The labeled protein is unimpaired in its ability to form **capsids**. Our d. map reveals a single undecagold cluster under each fivefold and quasi-sixfold vertex, connected to sites at either end of the undersides of the dimers. Considering the geometry of the vertices, the C termini must be more crowded at the fivefolds. Thus, a bulky C terminus would be expected to favor formation of the larger (T = 4) **capsids**, which have a greater proportion of quasi-sixfolds. **Capsids** assembled by expressing the full-length protein in Escherichia coli package bacterial RNAs in amts. equiv. to the viral pregenome. Our d. map of these **capsids** reveals a distinct inner shell of d. - the RNA. The RNA is connected to the protein shell via the C-terminal linkers and also makes contact around the dimer axes.

L25 ANSWER 8 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 6
ACCESSION NUMBER: 1997:744679 CAPLUS
DOCUMENT NUMBER: 128:72117
TITLE: Hexon-only binding of VP26 reflects differences between the hexon and penton conformations of

VP5, the major **capsid** protein of herpes simplex virus

AUTHOR(S): **Wingfield, Paul T.**; Stahl, Stephen J.; Thomsen, Darrell R.; Homa, Fred L.; Booy, Frank P.; Trus, Benes L.; **Steven, Alasdair C.**

CORPORATE SOURCE: Protein Expression Laboratory, Division Computer Research and Technology, National Institute Arthritis and Musculoskeletal and Skin Diseases, and Computational Bioscience and Engineering Laboratory, National Institutes Health, Bethesda, MD, 20892, USA

SOURCE: J. Virol. (1997), 71(12), 8955-8961
CODEN: JOVIAM; ISSN: 0022-538X

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB VP26 is a 12-kDa **capsid** protein of herpes simplex virus 1. Although VP26 is dispensable for assembly, the native **capsid** (a T=16 icosahedron) contains 900 copies: six on each of the 150 hexons of VP5 (149 kDa) but none on the 12 VP5 pentons at its vertices. We have investigated this interaction by expressing VP26 in Escherichia coli and studying the properties of the purified protein in soln. and its binding to **capsids**. CD spectroscopy reveals that the conformation of purified VP26 consists mainly of .beta.-sheets (.apprx.80%), with a small .alpha.-helical component (.apprx.15%). Its state of assocn. was detd. by anal. ultracentrifugation to be a reversible monomer-dimer equil., with a dissocn. const. of .apprx.2.times.10-5 M. Bacterially expressed VP26 binds to **capsids** in the normal amt., as detd. by quant. SDS-PAGE. Cryoelectron microscopy shows that the protein occupies its usual sites on hexons but does not bind to pentons, even when available in 100-fold molar excess. Quasi-equivalence requires that penton VP5 must differ in conformation from hexon VP5: our data show that in mature **capsids**, this difference is sufficiently pronounced to abrogate its ability to bind VP26.

L25 ANSWER 9 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 7

ACCESSION NUMBER: 1997:174431 CAPLUS

DOCUMENT NUMBER: 126:274302

TITLE: Visualization of a 4-helix bundle in the hepatitis B virus **capsid** by cryo-electron microscopy

AUTHOR(S): Conway, J. F.; Cheng, N.; Zlotnick, A.; **Wingfield, P. T.**; Stahl, S. J.; **Steven, A. C.**

CORPORATE SOURCE: Lab. Structural Biology, National Inst. Health, Bethesda, MD, 20892, USA

SOURCE: Nature (London) (1997), 386(6620), 91-94
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Macmillan Magazines
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Despite the development of vaccines, the hepatitis B virus remains a major cause of human liver disease. The virion consists of a lipoprotein envelope surrounding an icosahedral **capsid** composed of dimers of a 183-residue protein, 'core antigen' (HBcAg). Knowledge of its structure is important for the design of antiviral drugs, but it has yet to be detd. Residues 150-183 are known to form a protamine-like domain required for packaging RNA, and residues 1-149 form the 'assembly domain' that polymerizes into **capsids** and, unusually for a **capsid** protein, is highly .alpha.-helical. The d. maps calcd. from cryo-electron micrographs show that the assembly domain dimer is T-shaped: its stem constitutes the dimer interface and the tips of its arms make the polymn. contacts. By refining the procedures used to calc. the map, we extended the resoln. to 9 .ANG., revealing major elements of secondary structure. In particular, the stem, which protrudes as a spike on the **capsid**'s outer surface, is a 4-helix bundle, formed by the pairing of .alpha.-helical hairpins from both subunits.

L25 ANSWER 10 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 8
ACCESSION NUMBER: 1996:304217 CAPLUS
DOCUMENT NUMBER: 124:335929
TITLE: Dimorphism of Hepatitis B Virus **Capsids** Is Strongly Influenced by the C-Terminus of the **Capsid** Protein
AUTHOR(S): Zlotnick, A.; Cheng, N.; Conway, J. F.; Booy, F. P.; **Steven, A. C.**; Stahl, S. J.; **Wingfield, P. T.**
CORPORATE SOURCE: Laboratory of Structural Biology, National Institute of Arthritis Musculoskeletal and Skin Diseases, Bethesda, MD, 20892, USA
SOURCE: Biochemistry (1996), 35(23), 7412-7421
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Hepatitis B virus (HBV) is an enveloped virus with an icosahedral **capsid**. Its homodimeric **capsid** protein ("core antigen") assembles into particles of two sizes, one with T = 3 icosahedral symmetry (90 dimers) and the other with T = 4 symmetry (120 dimers). We have investigated this assembly process in vitro, using a variety of purified, bacterially expressed, **capsid** proteins. All of our constructs lacked the predominantly basic C-terminal 34 amino acids of the full-length **capsid** protein (183 amino acids) and were further truncated to terminate at specific points between residues 138 and 149. While the smallest construct (138 residues) did not assemble into **capsids**,

those terminating at residue 140, and beyond, assembled into mixts. of T = 3 and T = 4 particles. The two kinds of **capsids** could be sepd. on sucrose gradients and did not interconvert upon protracted storage. The proportion of T = 3 **capsids**, assayed by sucrose gradient fractionation, anal. ultracentrifugation, and cryoelectron microscopy, was found to increase systematically with larger deletions from the C-terminus. The variant terminating at residue 149 formed .apprx.10% of T = 3 **capsids**, while the 140-residue protein produced .apprx.85% of this isomorph. For the 147-residue **capsid** protein, the structures of both **capsids** were detd. to 17 .ANG. resoln. by three-dimensional reconstruction of cryoelectron micrographs. In these d. maps, the boundaries of the constituent dimers can be clearly seen and the quaternary structures of the two **capsids** compared. The arrangement of dimers around their icosahedral five-fold axes is almost identical, whereas the quasi-six-fold arrangements of dimers are distinctly different.

L25 ANSWER 11 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 9
ACCESSION NUMBER: 1996:572778 CAPLUS
DOCUMENT NUMBER: 125:266696
TITLE: Phage display of intact domains at high copy number: a system based on **SOC**, the small outer **capsid** protein of bacteriophage T4
AUTHOR(S): Ren, Z. J.; Lewis, G. K.; **Wingfield, P. T.**; Locke, E. G.; **Steven, A. C.**; **Black, L. W.**
CORPORATE SOURCE: Department of Biological Chemistry, University of Maryland School of Medicine, Baltimore, MD, 21201, USA
SOURCE: Protein Sci. (1996), 5(9), 1833-1843
CODEN: PRCIEI; ISSN: 0961-8368
DOCUMENT TYPE: Journal
LANGUAGE: English
AB. Peptides fused to the coat proteins of filamentous phages have found widespread applications in antigen display, the construction of antibody libraries, and biopanning. However, such systems are limited in terms of the size and no. of the peptides that may be incorporated without compromising the fusion proteins' capacity to self-assemble. We describe here a system in which the mols. to be displayed are bound to pre-assembled polymers. The polymers are T4 **capsids** and polyheads (tubular **capsid** variants) and the display mols. are derivs. of the dispensable **capsid** protein **SOC**. In one implementation, **SOC** and its fusion derivs. are expressed at high levels in Escherichia coli, purified in high yield, and then bound in vitro to sep. isolated polyheads. In the other, a pos. selection vector forces integration of the modified **soc** gene into a **soc**-deleted T4

genome, leading to in vivo binding of the display protein to progeny virions. The system is demonstrated as applied to C-terminal fusions to **SOC** of (1) a tetrapeptide (Cys-Leu-Asn-Ser); (2) the 43-residue V3 loop domain of gp 120, the human immunodeficiency virus type-1 (HIV-1) envelope glycoprotein; and (3) poliovirus VP1 **capsid** protein (312 residues). **SOC** -V3 displaying phage were highly antigenic in mice and produced antibodies reactive with native gp 120. That the fusion protein binds correctly to the surface lattice was attested in averaged electron micrographs of polyheads. The **SOC** display system is capable of presenting up to .apprx.103 copies per **capsid** and >104 copies per polyhead of V3-sized domains. Phage displaying **SOC**-VP1 were isolated from a 1:106 mixt. by two cycles of a simple biopanning procedure, indicating that proteins of at lease 35 kDa may be accommodated.

L25 ANSWER 12 OF 20 BIOSIS COPYRIGHT 1999 BIOSIS DUPLICATE 10
ACCESSION NUMBER: 1996:261629 BIOSIS
DOCUMENT NUMBER: PREV199698817758
TITLE: Display of peptides, domains and proteins on **SOC**, the small outer **capsid** protein of bacteriophage T4.
AUTHOR(S): Ren, Z. J. (1); Lewis, G. (1); **Wingfield, P. T.**; Locke, E. G.; **Steven, A. C.**; **Black, L. W. (1)**
CORPORATE SOURCE: (1) Univ. Md. Sch. Med., Baltimore, MD 21201 USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (1996) Vol. 96, No. 0, pp. 576.
Meeting Info.: 96th General Meeting of the American Society for Microbiology New Orleans, Louisiana, USA May 19-23, 1996
ISSN: 1060-2011.
DOCUMENT TYPE: Conference
LANGUAGE: English

L25 ANSWER 13 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 11
ACCESSION NUMBER: 1995:495087 CAPLUS
DOCUMENT NUMBER: 122:233721
TITLE: Hepatitis Core Antigen Produced in Escherichia coli: Subunit Composition, Conformation Analysis, and in Vitro **Capsid** Assembly
AUTHOR(S): **Wingfield, Paul T.**; Stahl, Stephen J.; Williams, Robert W.; **Steven, Alasdair C.**
CORPORATE SOURCE: Protein Expression Laboratory, Office of the Director, Bethesda, MD, 20892-2775, USA
SOURCE: Biochemistry (1995), 34(15), 4919-32
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal

LANGUAGE: English

AB The prodn. and biochem. and physicochem. anal. are described of recombinant-produced hepatitis B virus core antigen (HBcAg **capsid**) and the corresponding particle produced by a deletion mutant missing the C-terminal 39 residues (HBeAg). Conditions for producing HBeAg from HBcAg **capsids** by in vitro proteolysis are also described. The morphol. and masses of these **capsids** were detd. by scanning transmission electron microscopy. Both HBcAg and HBeAg **capsids** comprise two size classes that correspond to icosahedral lattices with triangulation nos. (T) of 3 and 4, contg. 180 and 240 subunits per **capsid**, resp. This dimorphism was confirmed by sedimentation equil. and sedimentation velocity measurements on a Beckman Optima XL-A anal. ultracentrifuge. More than 60% of HBcAg **capsids** were T = 4, whereas only 15-20% of HBeAg **capsids** were of this size class: the remainder, in each case, were T = 3. CD and Raman spectroscopy were used to det. the overall secondary structures of HBcAg and HBeAg **capsids**. Both have high .alpha.-helical contents, implying that this **capsid** protein does not conform to the canonical .beta.-barrel motif seen for all plant and animal icosahedral viral **capsids** solved to date. We suggest that the C-terminal domain of HBcAg has a random coil conformation. In vitro dissocn. of HBeAg **capsids** under relatively mild conditions yielded stable dimers. The reassocn. of HBeAg dimers into **capsids** appears to be driven by hydrophobic processes at neutral pH. **Capsid** assembly is accompanied by little change in subunit conformation as judged by CD and fluorescence spectroscopy. The thermal stability of HBcAg **capsids** was compared calorimetrically with that of the in vitro assembled HBeAg **capsids**. Both have melting temps. >90 .degree.C, implying that the C-terminal region makes little difference to the thermal stability of HBcAg: nevertheless, we discuss its possible role in facilitating disassembly and the release of viral nucleic acid.

L25 ANSWER 14 OF 20 BIOSIS COPYRIGHT 1999 BIOSIS
ACCESSION NUMBER: 1995:694 BIOSIS
DOCUMENT NUMBER: PREV199598014994
TITLE: Morphogenesis of the T4 head.
AUTHOR(S): **Black, Lindsay W. (1)**; Showe, Michael K.; **Steven, Alasdair C.**
CORPORATE SOURCE: (1) Dep. Biological Chemistry, Univ. Md. Sch. Med., 660 West Redwood Street, Baltimore, MD 21201 USA
SOURCE: Karam, J. D. [Editor]. (1994) pp. 218-258. Molecular biology of bacteriophage T4.
Publisher: American Society for Microbiology (ASM) Books Division, 1325 Massachusetts Ave. NW, Washington, DC 20005-4171, USA.
ISBN: 1-55581-064-0.

DOCUMENT TYPE: Book
LANGUAGE: English

L25 ANSWER 15 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 12
ACCESSION NUMBER: 1993:54666 CAPLUS
DOCUMENT NUMBER: 118:54666
TITLE: Conformational changes of a viral **capsid** protein. Thermodynamic rationale for proteolytic regulation of bacteriophage T4 **capsid** expansion, cooperativity, and super-stabilization by **Soc** binding
AUTHOR(S): **Steven, Alasdair C.**; Greenstone, Heather L.; Booy, Frank P.; **Black, Lindsay W.**; Ross, Philip D.
CORPORATE SOURCE: Lab. Struct. Biol., Natl. Inst. Arthritis Musculoskeletal Skin Dis., Bethesda, MD, 20892, USA
SOURCE: J. Mol. Biol. (1992), 228(3), 870-84
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Differential scanning calorimetry was used in conjunction with cryo-electron microscopy to investigate the conformational transitions undergone by the maturing **capsid** of phage T4. Its precursor shell is composed primarily of gp23 (521 residues): cleavage of gp23 to gp23* (residues 66 to 521) facilitates a concerted conformational change in which the particle expands substantially, and is greatly stabilized. The intermediate states of **capsid** maturation have now been characterized; namely, the cleaved/unexpanded, state, which denatures at tm = 60.degree., and the uncleaved/expanded state, for which tm = 70.degree.. When compared with the precursor uncleaved/unexpanded state (tm = 65.degree.), and the mature cleaved/expanded state (tm = 83.degree., if complete cleavage precedes expansion), it follows that expansion of the cleaved precursor (.DELTA.tm .apprx. +23.degree.) is the major stabilizing event in **capsid** maturation. These observations also suggest an advantage conferred by **capsid** protein cleavage (some other phage **capsids** expand without cleavage): if the gp23.DELTA. domains (residues 1 to 65) are not removed by proteolysis, they impede formation of the stablest possible bonding arrangement when expansion occurs, most likely by becoming trapped at the interface between neighboring subunits or capsomers. Icosahedral **capsids** denature at essentially the same temps. as tubular polymorphic variants (polyheads) for the same state of the surface lattice. However, the thermal transitions of **capsids** are considerably sharper, i.e. more co-operative, than those of polyheads, which we attribute to **capsids** being closed, not open-ended. In both cases, binding of the accessory protein **soc** around the threefold

sites on the outer surface of the expanded surface lattice results in a substantial further stabilization (.DELTA.tm = +5.degree.). The interfaces between capsomers appear to be relatively weak points that are reinforced by clamp-like binding of **soc**. These results imply that the triplex proteins of other viruses (their structural counterparts of **soc**) are likely also to be involved in **capsid** stabilization. Cryo-electron microscopy was used to make conclusive interpretations of endotherms in terms of denaturation events. These data also revealed that the cleaved/unexpanded **capsid** has an angular polyhedral morphol. and has a pronounced relief on its outer surface. Moreover, it is 14% smaller in linear dimensions than the cleaved/expanded **capsid**, and its shell is commensurately thicker.

L25 ANSWER 16 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 13
ACCESSION NUMBER: 1991:531706 CAPLUS
DOCUMENT NUMBER: 115:131706
TITLE: The maturation-dependent conformational change of phage T4 **capsid** involves the translocation of specific epitopes between the inner and the outer **capsid** surfaces
AUTHOR(S): **Steven, Alasdair C.**; Bauer, Adelia C.; Bisher, Margaret E.; Robey, Frank A.; **Black, Lindsay W.**
CORPORATE SOURCE: Lab. Struct. Biol. Res., Natl. Inst. Arthritis, Musculoskeletal, Skin Dis., Bethesda, MD, 20892, USA
SOURCE: J. Struct. Biol. (1991), 106(3), 221-36
CODEN: JSBIEM; ISSN: 1047-8477
DOCUMENT TYPE: Journal
LANGUAGE: English
AB After polymn. of the phage T4 prohead is complete, its **capsid** expands by .apprx.16%, is greatly stabilized, and acquires the capacity to bind accessory proteins. These effects are manifestations of a large-scale, irreversible, conformational change undergone by the major **capsid** protein, gp23 (521 residues) which is cleaved to gp23* (residues 66-521) during the maturation process. In order to explore its structural basis, immunoelectron microscopy was performed with antibodies raised against synthetic peptides that correspond to precisely defined segments of the amino acid sequence of gp23. These antibodies were used to label purified polyheads (tubular polymorphic variants of the normal icosahedral **capsid**), in expts. designed to impose constraints on the possible foldings of the gp23/gp23* polypeptide chains in their successive conformational states. Peptide 1 (residues 48-57), part of the gp23-.DELTA. domain that is excised when gp23 is converted to gp23*, resides on the inner surface of the precursor surface lattice, but if not proteolyzed, is found on the outer surface of

the mature surface lattice. Peptide 2 (residues 65-73), immediately distal to the cleavage site, is located on the inside of the precursor surface lattice, and remains there subsequent to expansion. Peptide 3 (residues 139-146) is translocated in the opposite direction from peptide 1, i.e., from the outer to the inner surface upon expansion; moreover, expansion greatly increases the polyheads' affinity for these antibodies. Peptide 5 (residues 301-308) is located on the inside in both the precursor and the mature states. Apparently, the conformational change that underlies **capsid** expansion involves a radical reorganization of the proteins' structure, in which at .gtoreq.3 distinct epitopes, situated in widely differing parts of the polypeptide chain, are translocated from one side to the other. Moreover, the amino-terminal portion of gp23/gp23*, around the cleavage site, is particularly affected.

L25 ANSWER 17 OF 20 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 14
ACCESSION NUMBER: 1985:450955 CAPLUS
DOCUMENT NUMBER: 103:50955
TITLE: Assembly-dependent conformational changes in a viral **capsid** protein. Calorimetric comparison of successive conformational states of the gp23 surface lattice of bacteriophage T4
AUTHOR(S): Ross, Philip D.; **Black, Lindsay W.**; Bisher, Margaret E.; **Steven, Alasdair C.**
CORPORATE SOURCE: Lab. Mol. Biol., Natl. Inst. Arthritis, Diabetes Dig. Kidney Dis., Bethesda, MD, 20205, USA
SOURCE: J. Mol. Biol. (1985), 183(3), 353-64
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Inter- and intrasubunit bonding within the surface lattice of the **capsid** of bacteriophage T4 was investigated by differential scanning calorimetry of polyheads, in conjunction with electron microscopy, limited proteolysis, and SDS-polyacrylamide gel electrophoresis. The bonding changes corresponding to successive stages of assembly of the major **capsid** protein gp23, including its maturation cleavage, were similarly characterized. The uncleaved/unexpanded surface lattice exhibited 2 endothermic transitions. The minor event, at 46.degree., did not visibly affect the surface lattice morphol. and probably represents denaturation of the N-terminal domain of gp23. The major endotherm, at 65.degree., represents denaturation of the gp23 polymers. Sol. gp23 from dissocd. polyheads was extremely unstable and exhibited no endotherm. Cleavage of gp23 to gp23* and the ensuing expansion transformation effected a major stabilization of the surface lattice of polyheads, with single endotherms whose m.p. (tm*) ranged 73-81.degree. depending upon the mutant used and the fraction of gp23 that was cleaved to gp23* prior to expansion. Binding of the

accessory proteins **soc** and **hoc** further modulated the thermograms of cleaved/expanded polyheads, and their effects were additive. Binding of **hoc** conferred a new minor endotherm at 68.degree. corresponding to at least partial denaturation of **hoc**. Denatured **hoc** nevertheless remained assocd., with the surface lattice although in an altered, protease-sensitive state which correlated with delocalization of **hoc** subunits visualized in filtered images. While **hoc** binding had little effect on thermal stability of the gp23* matrix, **soc** binding further stabilized the surface lattice (.DELTA.Hd .apprx.+50%; .DELTA.tm* = +5.5.degree.). In all states of the surface lattice, the inter- and intrasubunit bonding configurations of gp23 appeared to be coordinated to be of similar thermal stability. Thermodynamically, the expansion transformation was characterized by .DELTA.H .mchlt. 0; .DELTA.Cp .apprx. 0, suggesting enhancement of van der Waals' and(or) H-bonding interactions, together with an increased exposure to solvent of hydrophobic residues of gp23* in the expanded state. These findings illuminate hypotheses of **capsid** assembly based on conformational properties of gp23: inter alia, they indicate a role for the N-terminal portion of gp23 in regulating polymn., and force a reappraisal of models of **capsid** swelling based on the swivelling of conserved domains.

L25 ANSWER 18 OF 20 CONFSCI COPYRIGHT 1999 CSA
ACCESSION NUMBER: 1999:37256 CONFSCI
DOCUMENT NUMBER: 99-049750
TITLE: Mapping sites on the surface of the hepatitis B virus **capsid** by cryo-electron microscopy with tetra-iridium clusters
AUTHOR: Cheng, N.; Conway, J.; Watts, N.; Hainfeld, J.; Stahl, S.J.; **Wingfield, P.**; **Steven, A.C.**; Miller, J.
CORPORATE SOURCE: NIAMS-NIH, Bethesda, MD, USA
SOURCE: Biophysical Society, 9650 Rockville Pike, Bethesda, MD 20814, USA; phone: (301) 530-7114; fax: (301) 530-7133; email: society@biophysics.faseb.org; URL: www.biophysics.faseb.org, Abstracts available. Price $25. Poster Paper.
Meeting Info.: 991 0048: 43rd Annual Meeting of the Biophysical Society (9910048). Baltimore, MD (USA). 13-17 Feb 1999. Biophysical Society.
DOCUMENT TYPE: Conference
FILE SEGMENT: DCCP
LANGUAGE: English

L25 ANSWER 19 OF 20 CONFSCI COPYRIGHT 1999 CSA
ACCESSION NUMBER: 97:3637 CONFSCI
DOCUMENT NUMBER: 97-015613

TITLE: Visualization and analysis of **capsid** dimorphism in hepatitis B virus to 17 angstrom resolution by cryo-electron microscopy
AUTHOR: Zlotnick, A.; Cheng, N.; Conway, J.F.; Booy, F.P.; **Steven, A.C.**; Stahl, S.J.; **Wingfield, P.T.**
CORPORATE SOURCE: Lab Structural Biol, NIH, Bethesda, MD, USA
SOURCE: San Francisco Press, Box 426800, San Francisco, CA 94142-6800, Abstracts available. Poster Paper.
Meeting Info.: 963 5006: Microscopy and Microanalysis '96 (9635006). Minneapolis, MN (USA). 11-15 Aug 1996. Microscopy Society of America; Microscopy Analysis Society; Microscopical Society of Canada.
DOCUMENT TYPE: Conference
FILE SEGMENT: DCCP
LANGUAGE: English

L25 ANSWER 20 OF 20 CONFSCI COPYRIGHT 1999 CSA
ACCESSION NUMBER: 97:51198 CONFSCI
DOCUMENT NUMBER: 97-063177
TITLE: Structural role of the C-terminus of hepatitis B virus **capsid** protein in **capsid** assembly and RNA organization
AUTHOR: Zlotnick, A.; Cheng, N.; Stahl, S.J.; Conway, J.F.; **Steven, A.C.**; **Wingfield, P.T.**
CORPORATE SOURCE: NIAMS-NIH, Bethesda, MD 20892, USA
SOURCE: The Protein Society, 9650 Rockville Pike, Bethesda, MD 20814-3998, Abstracts available. Price $24. Poster Paper No. 348-T.
Meeting Info.: 973 0380: 11th Symposium of the Protein Society (9730380). Boston, MA (USA). 12-16 Jul 1997. Affymax Research Institute; Chevron Corp.; Genencor International; Genetech Inc.; Glaxo-Wellcome; Kabi Pharmaceuticals.
DOCUMENT TYPE: Conference
FILE SEGMENT: DCCP
LANGUAGE: English

=> d his l26-; d 1-4 ibib abs

(FILE 'CAPLUS, MEDLINE, BIOSIS, EMBASE, LIFESCI, BIOTECHDS, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, PROMT' ENTERED AT 16:16:11 ON 02 AUG 1999)
L26 1646 S REN Z?/AU
L27 27 S L26 AND (L16 OR L17 OR L18)
L28 20 S L27 NOT L24
L29 4 DUP REM L28 (16 DUPLICATES REMOVED)

Searcher : Shears 308-4994

L29 ANSWER 1 OF 4 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 1
ACCESSION NUMBER: 1998:590311 CAPLUS
DOCUMENT NUMBER: 129:286551
TITLE: Phage T4 SOC and HOC display of biologically active, full-length proteins on the viral capsid
AUTHOR(S): **Ren, Zhao-Jun; Black, Lindsay W.**
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Maryland School of Medicine, Baltimore, MD, 21201-1503, USA
SOURCE: Gene (1998), 215(2), 439-444
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The T4 phage capsid accessory protein genes soc and hoc have recently been developed for display of peptides and protein domains at high copy no. That biol. active and full-length foreign proteins can be displayed by fusion to SOC and HOC on the T4 capsid is demonstrated in this report. A 271-residue heavy and light chain fused IgG anti-EWL (egg white lysozyme) antibody was displayed in active form attached to the COOH-terminus of the SOC capsid protein, as demonstrated by lysozyme-agarose affinity chromatog. (> 100-fold increase in specific titer). HOC with NH2-terminal fused HIV-I CD4 receptor of 183 amino acids can be detected on the T4 outer capsid surface with human CD4 domain 1 and 2 monoclonal antibodies. The no. of mols. of each protein (10-40) bound per phage and their activity suggest that proteins can fold to native conformation and be displayed by HOC and SOC to allow binding and protein-protein interactions on the capsid.

L29 ANSWER 2 OF 4 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 2
ACCESSION NUMBER: 1997:504777 CAPLUS
DOCUMENT NUMBER: 127:215644
TITLE: Cloning of linear DNAs in vivo by overexpressed T4 DNA ligase: construction of a T4 phage hoc gene display vector.
AUTHOR(S): **Ren, Z. J.**; Baumann, R. G.; **Black, L. W.**
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Maryland School of Medicine, Baltimore, USA
SOURCE: Gene (1997), 195(2), 303-311
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

Searcher : Shears 308-4994

AB A method was developed to clone linear DNAs by overexpressing T4 phage DNA ligase in vivo, based upon recombination deficient E. coli derivs. that carry a plasmid contg. an inducible T4 DNA ligase gene. Integration of this ligase-plasmid into the chromosome of such E. coli allows std. plasmid isolation following linear DNA transformation of the strains contg. high levels of T4 DNA ligase. Intramol. ligation allows high efficiency recircularization of cohesive and blunt-end terminated linear plasmid DNAs following transformation. Recombinant plasmids could be constructed in vivo by co-transformation with linearized vector plus insert DNAs, followed by intermol. ligation in the T4 ligase strains to yield clones without deletions or rearrangements. Thus, in vitro packaged lox-site terminated plasmid DNAs injected from phage T4 were recircularized by T4 ligase in vivo with an efficiency comparable to CRE recombinase. Clones that expressed a capsid-binding 14-aa N-terminal peptide extension deriv. of the HOC (highly antigenic outer capsid) protein for T4 phage hoc gene display were constructed by co-transformation with a linearized vector and a PCR-synthesized hoc gene. Therefore, the T4 DNA ligase strains are useful for cloning linear DNAs in vivo by transformation or transduction of DNAs with nonsequence-specific but compatible DNA ends.

L29 ANSWER 3 OF 4 CAPLUS COPYRIGHT 1999 ACS DUPLICATE 3
ACCESSION NUMBER: 1997:95229 CAPLUS
DOCUMENT NUMBER: 126:166950
TITLE: A powerful approach for generating and sequencing DNA deletions: sequencing from the outside in
AUTHOR(S): **Ren, Zhaojun**; Nie, Wenxian; **Black, Lindsay W.**
CORPORATE SOURCE: School of Medicine, University of Maryland, Baltimore, MD, 21201-1503, USA
SOURCE: Anal. Biochem. (1997), 245(1), 112-114
CODEN: ANBCA2; ISSN: 0003-2697
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English

AB For large DNA fragment sequencing, construction of a nested DNA deletion series is an efficient method. A no. of methods are available for generating unidirectional deletions of a target fragment based on nuclease digestion. A bidirectional deletion and sequencing approach from "inside out" has also been developed, where the target fragment should be carried on a plasmid and ligated to a sequencing linker. Presented here is a different bidirectional nested deletion approach proceeding from both ends on a target DNA fragment, i.e., from "outside in.". In this protocol the target DNA can be produced from either a plasmid or a PCR product, and both exonuclease III and Bal31 can be utilized for shortening the target length to generated systematic nested deletions of between 150 and

300 nt from each end. In contrast to previously present methods, no sequences or restriction site information about the target DNA are required, and std. com. primers are sufficient.

L29 ANSWER 4 OF 4 BIOSIS COPYRIGHT 1999 BIOSIS
ACCESSION NUMBER: 1995:148483 BIOSIS
DOCUMENT NUMBER: PREV199598162783
TITLE: Groes homologue specifically required to fold the major capsid protein of phage T4 because of localized sequence determinants.
AUTHOR(S): Andreadis, Joanne D.; **Ren, Zhaojun**; **Black, Lindsay W.**
CORPORATE SOURCE: Dep. Biological Chemistry, Univ. Md. AT Baltimore, Baltimore, MD 21201 USA
SOURCE: Journal of Cellular Biochemistry Supplement, (1995) Vol. 0, No. 19B, pp. 208.
Meeting Info.: Keystone Symposium on Heat Shock (Stress) Proteins in Biology and Medicine Santa Fe, New Mexico, USA February 27-March 5, 1995
ISSN: 0733-1959.
DOCUMENT TYPE: Conference
LANGUAGE: English

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spans an origin of DNA replication.
Macdonald P M; Mosig G
NUMBER: GM 13221 (NIGMS)
RR07201 (NCRR)
T32 GM07319 (NIGMS)
SOURCE: EMBO JOURNAL, (1984 Dec 1) 3 (12) 2863-71.
Journal code: EMB. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-K03113
ENTRY MONTH: 198506

AB We have determined the DNA sequence and transcription patterns in a 3-kb segment (between 15 and 18 kb on the standard phage T4 map) spanning an origin of DNA replication. A new gene, 69, spans this origin. Gene 69 codes for two overlapping proteins that share a common C-terminal segment. Defective DNA replication in an appropriate amber mutant shows that at least the larger of the two proteins is required for efficient T4 DNA replication. The two proteins coded by gene 69 are expressed from different transcripts that are under different regulation. The smaller protein, gp69*, can be expressed immediately from an Escherichia coli-like promoter, whereas expression of the larger protein, gp69, must be delayed since its middle promoter requires T4 coded proteins, most likely gp mot, for activation. We discuss the possible significance of two overlapping proteins in the assembly of replisomes. Gene 69 is bracketed by the non-essential early gene dam (DNA adenine methylase) and the late gene **soc** (**small** outer **capsid** protein). Transcripts through this region are interdigitated in a complex pattern, which reveals all elements that are thought to be important in regulation of pre-replicative and post-replicative T4 genes.

L8 ANSWER 25 OF 27 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 84266136 MEDLINE
DOCUMENT NUMBER: 84266136
TITLE: Interaction of reovirus with cell surface **receptors**. IV. The reovirus type 3 **receptor** is expressed predominantly on murine Lyt-2,3+ and human T8+ cells.
AUTHOR: Epstein R L; Finberg R; Powers M L; Weiner H L
CONTRACT NUMBER: NSAI-16998
NIAID-16701
SOURCE: JOURNAL OF IMMUNOLOGY, (1984 Sep) 133 (3) 1614-7.
Journal code: IFB. ISSN: 0022-1767.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

[redacted] strain. 3 Target sequences derived from the [redacted] region were amplified after 2 rounds of the [redacted] chain reaction. Glutathione-S-transferase (GST, [redacted]-capsid fusions were constructed by inserting [redacted] segments of the capsid gene into the GST fusion vector [redacted] pGEX-3X. To further delineate the location of seroreactive [redacted] topes within the capsid protein, 3 **smaller** GST-[redacted] fusions were constructed by inserting sets of [redacted] ynthetic oligonucleotides encoding 20 **amino** acid [redacted] proteins into the GST fusion vector plasmid pGEX-2T. The various fusion proteins were expressed in Escherichia coli W3110 and total cell lysates were analyzed by SDS-PAGE. Expression of the capsid fusion proteins varied from 17% to 31% of total cell protein. An immunodominant epitope was located within the N-terminal portion of capsid that was preferentially recognized by **antibodies** in both human and chimpanzee HCV-positive sera. These fusion proteins may be of use in the development of specific tests for blood screening and clinical diagnosis of HCV. (20 ref)

L8 ANSWER 23 OF 27 BIOSIS COPYRIGHT 1999 BIOSIS DUPLICATE 9
ACCESSION NUMBER: 1988:140084 BIOSIS
DOCUMENT NUMBER: BA85:74911
TITLE: ISOLATION AND ANTIGENIC CHARACTERIZATION OF DENSE PARTICLES OF SWINE ENTEROVIRUSES.
AUTHOR(S): URAKAWA T; HAMADA N; SHINGU M
CORPORATE SOURCE: DEP. VIROL., KURUME UNIV. SCH. MED., KURUME, 830 JPN.
SOURCE: KURUME MED J, (1987) 34 (2), 65-74.
CODEN: KRMJAC. ISSN: 0023-5679.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Dense particles (buoyant density in CsCl: 1.45-1.47 g/cm3) were isolated from HeLa cells infected with swine enteroviruses and coxsackievirus type B5. These dense particles had important properties which were different from those of poliovirus and other picornaviruses described previously; for instance, they could be isolated under various conditions of virus growth. The **smallest capsid polypeptide**, VP4, was not detected by SDS-PAGE analysis. The preparations of dense particels were non-infectious and showed H antigenicity by a modified **enzyme** immunoassay. Judging from these properties, dense particles might be equivalent to "A particles". These findings suggest that the VP4 **polypeptide** is responsible for the conformational stabilization of the intact virion.

L8 ANSWER 24 OF 27 MEDLINE
ACCESSION NUMBER: 85126881 MEDLINE
DOCUMENT NUMBER: 85126881
TITLE: Regulation of a new bacteriophage T4 gene, 69, that

26 ANSWER 4 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 4
AN 1997:515453 BIOSIS
DN PREV199799814656
TI **Display** for a PorA peptide from Neisseria meningitidis on the bacteriophage **T4** capsid surface.
AU Jiang, Jennifer; Abu-Shilbayeh, Lara; Rao, Venigalla B. (1)
CS (1) Dep. Biol., 103 McCort Ward Hall, Catholic Univ. America, 620 Michigan Ave. NE, Washington, DC 20064 USA
SO Infection and Immunity, (1997) Vol. 65, No. 11, pp. 4770-4777. ISSN: 0019-9567.
DT Article
LA English
AB The exterior of bacteriophage **T4** capsid is coated with two outer capsid proteins, Hoc (highly antigenic outer capsid protein; molecular mass, 40 kDa) and **Soc** (small outer capsid protein; molecular mass, 9 kDa), at symmetrical positions on the icosahedron (160 copies of Hoc and 960 copies of **Soc** per capsid particle). Both these proteins are nonessential for phage infectivity and viability and assemble onto the capsid surface after completion of capsid assembly. We developed a phage **display** system which allowed in-frame fusions of foreign DNA at a unique cloning site in the 5' end of hoc or **soc**. A DNA fragment corresponding to the 36-amino-acid PorA peptide from Neisseria meningitides was cloned into the **display** vectors to generate fusions at the N terminus of Hoc or **Soc**. The PorA-Hoc and PorA-**Soc** fusion proteins retained the ability to bind to the capsid surface, and the bound peptide was **displayed** in an accessible form as shown by its reactivity with specific monoclonal antibodies in an enzyme-linked immunosorbent assay. By employing **T4** genetic strategies, we show that more than one subtype-specific PorA peptide can be **displayed** on the capsid surface and that the peptide can also be **displayed** on a DNA-free empty capsid. Both the PorA-Hoc and PorA-**Soc** recombinant phages are highly immunogenic in mice and elicit strong antipeptide antibody titers even with a weak adjuvant such as Alhydrogel or no adjuvant at all. The data suggest that the phage **T4** hoc-**soc** system is an attractive system for **display** of peptides on an icosahedral capsid surface and may emerge as a powerful system for construction of the next generation multicomponent vaccines.
CC Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Physiology and Biochemistry of Bacteria *31000
Virology - Bacteriophage *33504
Immunology and Immunochemistry - Bacterial, Viral and Fungal *34504
Immunology and Immunochemistry - Immunopathology, Tissue Immunology *34508
Medical and Clinical Microbiology - Bacteriology *36002
BC Myoviridae 02707
Neisseriaceae *06507
IT Major Concepts
Biochemistry and Molecular Biophysics; Immune System (Chemical Coordination and Homeostasis); Infection; Microbiology; Physiology
IT Miscellaneous Descriptors
CAPSID SURFACE; DNA; HIGHLY ANTIGENIC; HOC; IMMUNE SYSTEM; INFECTION; MULTICOMPONENT VACCINE; OUTER CAPSID PROTEIN; OUTER CAPSID PROTEINS; PORA PEPTIDE; **SOC**
ORGN Super Taxa
Myoviridae: Viruses; Neisseriaceae: Eubacteria, Bacteria
ORGN Organism Name
bacteriophage **T4** (Myoviridae); Neisseria meningitidis (Neisseriaceae)
ORGN Organism Superterms
bacteria; eubacteria; microorganisms; viruses

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ORGN Super Taxa
Myoviridae: Viruses; Neisseriaceae: Eubacteria, Bacteria
ORGN Organism Name
bacteriophage **T4** (Myoviridae); Neisseria meningitidis (Neisseriaceae)
ORGN Organism Superterms
bacteria; eubacteria; microorganisms; viruses